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 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                     Query Match 100.0%; Score 1269; DB 6; Best Local Similarity 100.0%; Pred. No. 6.9e-254; Matches 1269; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                Patent: JP 2002542826-A 1 17-DEC-2002;
Avantis Pharmaceuticals Products Inc,George H Searfoss III, Marco F Pagnoni,Yuri D Ivashchenko,Kun Guo,Kenneth L Clark OS Homo sapiens PN JP 2002542826-A/1
PD 17-DEC-2002
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PR 30-APR-1299 US 60/131940
PI yuri d ivashchenko,george h searfoss iii,marco f pagnoni,kun PI kenneth l clark
CC
FH Key Lication/Qualifiers.
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1 (bases 1 to 1269)

Ivashchenko, Y.D., Iii, G.H.S., Pagnoni, M.F., Guo, K. and Clark, K.L. VARIANTS OF TRAF2 WHICH ACT AS AN INHIBITOR OF TNF-ALPHA SIGNALING
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polyA_signal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Newherberg, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by MediGenomix (Martinsried/Germany) within the cDNA
sequencing consortium of the German Genome Project. This clone
(DKFZp686H1465) is available at the RZPD in Berlin. Please contact
the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANy; Email: clone@rzpd.de Further
information about the clone and the sequencing project is available
at http://mips.gsf.de/proj/cDNA/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            בעהמוץOta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases to 2244)
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                                                                                                                                                                                                                                                                                                                                   note="TNF
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Fobo,G., Han,M. an
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n clone DKFZp686H1465);
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	REFERENCE AUTHORS TITLE JOURNAL	39 AGGAGCATTGGCCTCAAGGACCTGGCGATGGCTGACTTGGAGCAGAAAGGTCTTGGAGATG 7	Q D Q
human and mouse cDNA sequence Proc. Natl. Acad. Sci. U.S.A. 12477932	JOURNAL	679 CAGCACCGGCTGGACCAAGACAAGATTGAAGCCCTGAGTAGCAAGGTGCAGCAGCTGGAG 738	B 8
Dickson, M.C., Rodriguez, A.C., Butterfield, Y.S., Krzywinski, Schnerch, A., Schein, J.E., Generation and initial analy	TITLE	619 GTCTGCGTCCTGAACCGGGAGGTGGAGAGGGTGGCCATGACTGCCGAGGCCTGCAGCCGG 678	אם מם
Villaion, D.K., Muzny, D.M., So Villaion, D.K., Ketteman Fahey, J., Helton, B., Ketteman Sanchez, A., Whiting, M., Madan Bouffard, G.G., Blakesley, R.W		559 TCAGAGCTCCTGCAGAGGTGCGAGAGCCTGGAGAAGAAGACGGCCACTTTTGAGAACATT 618	מס עס
Abramson, R.D., Mullahy, S.J., McKernan, K.J., Malek, J.A., Gworley, K.C., Hale, S., Garcia			Db 5
hopkins, K.F., Jordan, H., Moore, I Diatchenko, L., Marusina, K., Farme Stapleton, M., Soares, M.B., Bonald Scheetz, T.E., Brownstein, M.J., U Garrino: P Brance C Baha S,	· · · · ·	439 AUGUTAGAGGAGCAGAACAGCAGGAGCACGAGGTGCAGTGCCTGCGGGAGCACCTGGCC 498	\$ B &
Strausberg, K.L., Feingold, E.A., Klausner, R.D., Collins, F.S., Wagnaltschul, S.F., Zeeberg, B., Bueto		5 GTCAAGACTTGTGGCAAGTGTCGAGTCCCTTGCAGATTCCACGCCATCGGCTGCCTCGAG 67	g Db
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MGC. Homo sapiens (human) Momo sapiens	SOURCE ORGANISM	365AGTITCAGGACCAC 378	γQ
	ACCESSION VERSION	GGCCTGGTCCGCCTTGGTGAAAAGGAGCGCCACCTGGAGCACGAGTGCCCGGAGAGAAAGC	B 4
BC043492 Homo sapiens TNF receptor-associ	LOCUS	GAGAGCTGCCACGAAGGCCGCTGCCCGCTCATGCTGACCGAATGTCCCGCGTGCAA	B B
	RESULT 3 BC043492	361 TACG 364	Q
1455 CGGGACGATGCCATCTTCATCAAGGCCATT		301 GAGAGCCTGCCGGCCGTCTGTCCCAGTGATGGATGCACCTGGAAGGGGGACCCTGAAAGAA 360 	B 64
1395 GCAAGGGCTGCCCCTCTTCTGCCCCGTC	OV 1	241 GGCATTI CIATTITIAGAANGCAGTICGGCCTICCCAGAINATGCTGCCCGCAGGAAGGIG 300	95 A
1335 GCCTTCAGGCCCGACGTGACTTCATCCTCT 1359 GCAAGCGGCTGCCCCCTCTTCTGCCCCCGTC		ATCCTCAGCTCTGGGCCTCACAACTGTGCTGCCTGTGTTCACGAGGCCATATATCAAGAA 1 HILLIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHI	, B &
		195 CTCCGCAGGCCCTTCCAGGCGCAGTGTGGCCACCGGTACTGCTTCTTGTCTTGCCTAGCCAGC 254	Db
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JOURNAL PUBMED REFERENCE AUTHORS TITLE JOURNAL	UTH		Qy 1:	Qy 1:	Qу 1:	Оу 1: 1:	Ду 1:	Qy Db 1:	Db 04	ь
tial analysis of more than 15,00 MA sequences Sci. U.S.A. 99 (26), 16899-16903 Patient Institutes of Head CO., Cancer Genomics Office, Nater Drive, Room 11A03, Bethesda,	s, 1 to 2298) g,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler, S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,F.N., R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.N., Coll, Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., M., Soares,M.B., Bonaldo,M.F., Toshiyuki,S., P., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., P., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., M.J., Malek,J.A., Gunaratne,P.H., Richards,S., K.J., Malek,J.A., M., Gunaratne,P.H., Richards,R., K.J., Malek,J.A., M., Malek,J., Male	BC043492 Homo sapiens MGC:49872 IMP BC043492 BC043492.1 G MGC Homo sapiens Homo sapiens Eukaryota; Me Mammalia; But	219 CGGGACGATGCCATCTTCATCAAGGCCATTGTGGACCTGACAGGGCTCTAA 1269 	159 GCAAGCGGCTGCCCCCTCTTCTGCCCCGTCTCCAAGATGGAGGCAAAGAATTCCTACGTG 1218	099 GCCTTCAGGCCCGACGTGACTTCATCCTCTTTTCAGAGGCCAGTCAACGACATGAACATC 1158	039 TTCAACCAGAAGGTGACCTTAATGCTGGTCGACCAGAATAACCGGGAGGACGTGATTGAC 1098	979 CACCTGTCCCTCTTCTTGTGGGTGATGAAGGGCCCGAATGACGCCCTGCTGCGGTGGCCC 1038	919 TACGGCTACAAGATGTGTCTGCGTATCTACCTGAACGGCGACGGCACCGGGGGAGGAACA 978	859 CAGGAAGCTGTGGCTGGCCGCATACCCGCCATCTTCTCCCCAGCCTTCTACACCAGCAGG 918	

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NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-romail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,

"""" RC. Canada
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Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield,
Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth
Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth
Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao,
Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin,
Teika Olson, Diana Palmquist, Anca Petrescu, Anna Liisa Prahbu,
Parvaneh Saeedi, JR Santos, Angelique Schnerch, Ursula Skalaka,
Duane Smailus, Jeff Stott, Miranda Tsai, George Yang, Jacquie
Schein, Asim Siddiqui, Rob Holt, Marco Marra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNI at: http://image.llnl.gov Series: IRAK Plate: 89 Row: j Column. This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 22027611.
                                                                                                                         AAGACCCTCCTGGGGACCAAGCTGGAAGCCAAGTACCTGTGCTCCGCCTGCAGAAACGTC
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                                                                                   AAGACCCTCCTGGGGACCAAGCTGGAAGCCAAGTACCTGTGCTCCGCCTGCAGAAACGTC
                                                                                                                                                                                                                                                          Conservative
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HAIGCLETVEGEKQQEHEVQWLREHLAMLLSSVLEAKPLLGDQSHAGSBLLQRCESLE
                                                                                                                                                                                                                                                                                                                                                                               KKTATFENI VCVLNREVERVAMTAEACSRQHRLDQDKI EALSSKVQQLERSIGLKDLA
MADLEQKVLEMEASTYDGVFIWKI SDFARKRQEAVAGRI PAI F8PAFYTSRYGYKMCL
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/db_xref="LocusID:7186"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene="TRAF2"
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                                                                                                                                                                                                                                                                          80.4%;
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Altschul, S.F., Zeeberg, B., Buetow, K.H., Scheafer, C.M., Schuler, G.D.,
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human and mouse oDNA sequences
L. Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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                                   CTGCTGCGGTGGCCCTTCAACCAGAAGTGACCTTAATGCTGCTCGACCAGAATAACCGG 1377
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Homo sapiens TNF receptor-associated factor 2, mRNA (cDNA clone MGC:40274 IMAGE:5216790), complete cds.
  CTGCTGCGGTGGCCCTTCAACCAGAAGGTGACCTTAATGCTGCTCGACCAGAATAACCGG 1083
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Submitted (06-UTN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                        GAGCACGTGATTGACGCCTTCAGGCCCGACGTGACTTCATCCTCTTTTCAGAGGCCAGTC
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Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Web site: http://www.nisc.nih.gov/
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BC032410.1 GI:21619569
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MADLEQKVLEMEASTYDGVFIWKISDFARKROEAVAGRIPAIFSPAFYTSRYGYKMCL
RIYLMGDGTGRGTHLSLFFVVMKGPNDALLRWPFNQKVTLMLLDQNNREHVIDAFRPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 64 Row: 1 Column: 7 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 22027613. Location/Qualifiers
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Contact: nisc_mgc@nhgri.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffack,G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
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Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
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84.2%; Pred. No. 4e-202;
ive 0; Mismatches 1; Indels 237; Gaps
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/db_xref="MIM:601895"
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/db_xref="taxon:9606"
/clone="MGC:4024 IMAGE:5216790"
/tissue_type="Blood, adult leukocytes"
/clone_lib="NIH MGC_118"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"
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Matches 1268; Conservative
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	RESULT 5 BC033810 LOCUS LOCUS Homo sapiens TNF receptor-associated factor 2, mENA (cDNA clone DEFINITION MCC.45012 IMAGE:5182942); complete cds. ACCESSION BC033810 VERYWORDS RC33810.1 GI:21708063 KEYWORDS RC3810.1 GI:21708063 KEYWORDS RC4C1 Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. REFFERENCE LOBSES 1 to 2320) REFFERENCE Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Altschul, E.F., Jordan, H., Moore, T., Max,S.I., Wang,J., Hsieh,F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Scheetz, T.E., Brownstein, M.J., Usdin, T.E., Toshiyuki,S., Carninci, P., Prange, C., Raha, S. S., Loquellano, N.A., Peters, G.J., Abramenon, R.D., Mullahy,S.J., Bosak,S.A., McEwan, P.J., Morley, K.C., Hale,S., Garcia, A.M., Gay, L.J., Hulyk,S.W., Villalon, D.K., Whiting, M., Madan,A., Rodrigues,S., Fahey,J., Helton,E., Kettemen,M., Madan,A., Rodrigues,S., Ranchez,A., Whiting,M., Madan,A., Young,A., C., Shevchenko,Y., Fahey,J., Fahelton,E., Kettemen,M., Soung,A.C., Shevchenko,Y., Fahey,J., Fahelton,E., Kotteman,M., Rodrigues,S., Rodrigues,S., Shevchenko,Y., Fahey,J., Rodrigue,M., Young, Young,A., Young,A., C., Shevchenko,Y., Fahey,J., Rodrigue,A., Whiting,M., Madan,A., Young,A., Young,A., C., Shevchenko,Y., Fahey,J., Rodrigues,S.,	Bouffard, G.G., Blakeeley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J.W., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Schmutz, J., Wyers, R.W., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerci, A., Schein, J.T., Jones, S.J. and Marra, M.A. TITLE Generation and initial analysis of more than 15,000 full-length human and mouse CDNA sequences JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002) PUBNED 12477932 REFERENCE 2 (bases 1 to 2320) TITLE Direct Submission JOURNAL Gene Collection (NGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2890, USA REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov Contact: MGC help desk Email: cgapbs-remail.nih.gov Contact: MGC help desk Email: cgapbs-remail.nih.gov CONMENT Preparation: Life Technologies, Inc. CDNA Library Preparation: Maryland; Web site: http://www.nisc.nih.gov/ Contact: nisc_mgconhgri.nih.gov Contact: nisc_mgconhgri.nih.gov Contact: nisc_mgconhgri.nih.gov Akhter N., Ayele, K., Beckstrow-Sternberg, S.M., Benjamin, B., Blakesley, R. W., Benffard, G.G., Breen, K., Brinkley, C., Brooks, S., Blakesley, R. W., Benffard, G. G., Breen, K., Brinkley, C., Brooks, S., Blakesley, R. W., Bengfard, G. G., Breen, K., Brinkley, C., Brooks, S., Blakesley, R. W., Bengfard, G. G., Breen, K., Brinkley, C., Brooks, S., Blakesley, R. W., Bengfard, G. G., Breen, K., Brinkley, C., Brooks, S.,	Hansen,N., Ho, SL., Karinbs,E., Kwong,F., Larle,F., Legaspi,F., Maduro,O.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C., McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L., Young,A., Zhang,LH. and Green,B.D.
301 GAGAGCCTGCCGGCCGTCTCCCCAGTGATGCACCTGGAAGGGGACCCTGAAAGAA 360	365	### GAGGCCTGCAGCAGCAGCTGGACCAAGATTGAAGCCCTGAGTAGCAAG #################################	1084 GAGGACGTGATTGAGGCCTTCAGGCCCGACGTGACTTCATCCTTTTCAGAGGCCAGTC 1143

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| product="TRF receptor-associated factor 2"
| product="TRF receptor-associated factor 2"
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//lab_host="DH10E"
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAR Plate: 68 Row: 1 Column: 19
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 22027611.
Location/Qualifiers
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Pred. No. 4e-202;
0; Mismatches 1; Indels 237;
                                                                                                                                                                                                                                                                                                                                                         /gene="TRAF2"
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/dc_ref="MIM:601895"
                                                                                                                                                                                                                                                                                                                'note="Vector: pcmv-sport6"
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Best Local Similarity 84.2%;
Matches 1268; Conservative
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/traislation="WAAASTPPPGSIELLQPGFSKTLLGTKLEAKYLCSACRNVLRRP
FQACCHRYCSFCLASILSSGPONCAACVHEGISTESSSAFPDNAARREVES
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RIYLNGDGTGRGTHALELFVVMKGPNDALLAMPFNQKYTLMLLDQNNREHVIDAFRPD
VTSSSFQRFVNDMNIASGCPLFCPVSKMEAKNSYVRDDAIFKAIVDLTGL"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80.4%; Score 1020.4; DB 9;
84.2%; Pred. No. 3.8e-202;
tive 0; Mismatches 1;
           /gene="TRAF2"
/note="synonyms: TRAP3,
/db_xref="LocusID:7186"
/db_xref="MIM:601895"
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Matches 1268; Conservat
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Strausberg, N.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausher, R.L., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Morewason, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
Worley, K.C., Hale, S., Garcia, A.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Backer, J., Helten, B., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Voung, A.C., Shevchenko, Y.,
Butterfield, Y.S., Krzywinski, M.I., Skaiska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAK Plate: 110 Row: p Column: 2 This clone was elected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 22027611. Location/Qualifiers
                                                                                                               4893 bp mRNA linear PRI 30-JUN-2004 HOMO sapiens TNF receptor-associated factor 2, mRNA (cDNA clone MGC:60039 IMAGE:6528158), complete cds.
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 943
Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
R. M.
                                                                                                                                                                                                                                                                                                                                                   Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutele
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 4893)
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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Tissue Procurement: ATCC
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BC064662.1 GI:40352701
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Strausberg, R.
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Avantis Drawnacucicals Products Inc, George H Searfoss III, Marco F Pagnoni, Yuri D Ivashchenko, Kun Guo, Kenneth L Clark

OS Homo sapiens

PN UP 2002542826-A/2

PD 17-DEC-2002

PF 06-APR-2000 JP 2000615761

PR 30-APR-1999 US 60/131940

PI yuri divashchenko, george h searfoss iii, marco f pagnoni, kun PI guo,

PI kenneth I clark

CC

FH Key

Location/Qualifiers.
   Ivashchenko, Y. D., Iii, G.H.S., Pagnoni, M.F., Guo, K. and Clark, K.L. VARIANTS OF TRAF2 WHICH ACT AS AN INHIBITOR OF TNF-ALPHA SIGNALING
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Best Local Similarity 100.0%; Pred. No. 1.6e-199;
Matches 1008; Conservative 0; Mismatches 0;
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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VARIANTS OF TRAF2 WHICH ACT AS AN INHIBITOR OF TNF-ALPHA SIGNALING
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JP 200254826-A/2.
Homo sapiens (human)
Homo sapiens
Bukaryotas, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Bukaryota, Butheria; Primates; Catarrhini, Hominidae; Homo.
1 (bases 1 to 1011)
                                                                                                                     833 CAGAGCCACGCGGGGTCAGAGCTCCTGCAGAGGTGCGAGAGAGCCTGGAGAAGAAGAAGACGGCC
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664 GCCTACAAGATGTGTCTGCGTATCTACCTGAACGGCGACGGGGGGGG	982 CTGTCCTCTTCTTTGTGGTGATGAGGCCCGAATGACGCCCTGCTGCGGTGGCCCTTC 1041	1042 AACCAGAAGGTGACCTTAATGCTGGACCAGAATAACCGGGAGCACGTGATTGACGCC 1101 784 AACCAGAAGGTGACCTTAATGCTGCTCGAGAATAACCGGGAGCACGTGATTGACGCC 843	1102 TICAGGCCGACGIGACTICATCCTCTTTTCAGAGGCCAGTCAACGACATGAACATGGC 1161 	1162 AGGGCTGCCCCTTTTGCCCCGTCTCCAAGATGGAGGCAAAGAATTCCTACGTGCGG 1221	1222 GACGATGCATCTTCATCAAGGCCATTGTGGACCTGACAGGGCTCTAA 1269	964 GACGATCTTCATCAAGGCCATTGTGTGTTTTTTTTTTTT	RESULT 8 BD224867	z	receptor-associated ractor (TRAF), ACCESSION BD224867	-		AUINCES BAKEL, D. COWBELL, LOWELL, MONIA, B.F. AND AU,A.C. TITLE Antisense modulation of expression of tumor necrosis factor receptor-associated factor (TRRF)	JOURNAL Patent; JP 2002526095-A 2 20-AUG-2002; COMMENT OF HUMB CONTINENT OF HUMB CON		PR 06-OCT-1998 US 09/167109 PI BRENDA F BAKEN,LEX M COWSERT, BRETT P MONIA,XIAOXING S XU PC C12N15/09,A61X31/7105,A61X48/00,A61P29/00,A61P35/04,C12N15/00 CC Antisense modulation of expression of tumor necrosis factor CC	receptor-associated factor (TRAF) FH Key Location/Qualifiers FT CDS (55). FEATURES Location/Qualifiers	source 12262 /organism="Homo sapiens" /mol type="genomic DNA"	Later caxcing acco	Query Match 75.6%; Score 959.6; DB 6; Length 2262; Best Local Similarity 81.7%; Pred. No. 1.8e-189; Matches 1230; Conservative 0; Mismatches 39; Indels 237; Gaps 1;	1 ATGCTGCAGCTAGCGTGACCCCCCTGGCTCCCTGGAGTTGCTACAGCCCGGCTTCTCC 60		115 AAGACCCITCCIGGGGACCCAAGCIGGAAGCCAAGIACCIGIGCICCGCCIGCAGAAACGIC 1/4 121 CICCGCAGGCCCTTCCAGGCGCAGTGTGGCCACCGGTACTGCTCCTTCTGCCTGGCCAGC 180

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		1135 ATCCTCAGGAAGCTCAGGAAGCTGTGCCGCATACCCGCCATCTTCTCCCCAGCC 1194
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	10.5	RESULT 13 HSU12597 HSU12597 HSU12597 HUMAN LUMOR HUMOR DECOSIS factor type 2 receptor associated protein (TRAPA) mRNA, complete cds. JUESPON U12597 U125
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/ tanslation="MAAASVP96SLELLQPGFSKTLLGTKLEAKYLCSACRNVLRRP
FOAGGTRYCSFCLASTILSGPPONCAACVHEGTYEEGTSILESSSAPPDNAARREVES
LPAVCBSDGCTWKGTLKEYESCHEGROPLMATECPACKGIVRLGEKERHLEHECPERG
LESCHACRAPCGGADVKAHHEVCPKFPLTCDGCGKKIPPEKFQDHVKTCGKRVPCRF
HAIGGLEFYEGERQCGHEVOWAREHLAMLLSSYLEAKELLGOSHAGSELLQRCSELE
KKTATFENIVCVLNREVERVAMTAEACSRQHRLDQDKIEALLGSKVQQLERSIGKLDA
MADLEQKYRPQAGCGHEYOWARSALSTIRKLQBANGARIPATSRAFTSRYGYKMCL
MADLEQKYRPQAGCGHEYOWARSALSTIRKLQBANGARIPATSRAFTSRYGYKMCL
MADLEQKYRAFTENIVGKTATARREVERVANGANGALBANGARIPATISPAFTSRYGYKMCL
MADLEQKYRAFTENIVGKTATARREVTUDAFREV
                                                                                                                                                                           Song,H.Y.
Direct Submission

Birect Submission

Song, Physiology and Walther Oncology Center, Indiana University School of Medicine, 975 W. Walnut St., Indianapolis, IN 46202, USA

On Sep 6, 1995, this sequence version replaced gi:695148.
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         2 (bases 655 to 1560)
Rothe, M., Wong, S.C., Henzel, W.J. and Goeddel, D.V.
A novel family of putative signal transducers associated with the cytoplasmic domain of the 75 kDa tumor necrosis factor receptor Cell 78 (4), 681-692 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Areacrecaecraecerdacececereeereceredagarraeraeaeceeeerreee
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="TRAP3"
/note="TNF type 2 receptor binding protein"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note="cysteine-histidine rich region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note="encodes zinc finger-like motif"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 959.6; DB 9;
Pred. No. 1.8e-189;
0; Mismatches 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note="encodes ring finger motif"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          928. 1680
/gene="TRAP3"
/note="encodes TRAF domain"
/citation=[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="tumor necrosis
                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
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1...2262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /evidence=experimental
                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="TRAP3"
55. .1560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      154. .330
/gene="TRAP3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 579. .723
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/gene="TRAP3"
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Best Local Similarity 81.7%;
Matches 1230; Conservative
                                                                                                                                                              (bases 1 to 2262)
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	1203 Qy 410 GCAGATTCCAC	OY 430 INCCTICAGARGAGIAAGAAGAGAAGAAGAAGAAGAAGAAGAAGAAGAAGA	QY 544 CAGAGCCACGGGGGTCAGAGCTCCTGCAGAGGTGCGAGAAGACTGGAGAAGAAGACGGCCGAGAGCTGGAGAAGAAGACGCCGAGAGAGA	PAT 15-APR-2003 Qy 604 ACTITIGAGAACATIGICIGCGICCIGAACGGAGGIGGAGAGGGIGGCCAIGACIA	Qy 661	; Buteleostomi; DD 765 e; Homo.	ato,H., Ishii,S., Db 825 K., Irie,R., C., 766	QQ ·	Qy 826 ATCTGGAAGATCTCAGACTTCGCAGGAAGCTCCAGGAAGCTGTGCTGCCGCATACCC	Qy 886 GCCATCTTCTCCCCAGCCTTCTACACCAGGAGTACGGCTACAAGATGTGTCTGCGTATT 	Qy 946	2094; Db 1065 75; Gaps 6;	60 QY 1006 104 Db 1125	Qy	126 180 OY 1126 224 Db 1245	240 Qy 1186 284 Db 1305	Qy 1246 ATTGTGGACCTGTAA 1269	
1315 CTGCTGCGGTGGCCCTTCAACCAAAGGTGACCTTAATGCTGACCCAAATAACGGG 1084 GACCACGTGACCTTCAACCCAAGGTGACCTTAATGCTGACCTCAAACGGG 1087 GACCACGTTCAACCCCTTCAACCCCAAGGTGACTTAATCCTCTTTTCAAAGACCCAAGTC 1375 GACCAACGTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA		1204 AAGAATTCCTACGTGCGGACGATGCCATCTTCATCAAGGCCATTGTG	1555 CICIAA 1560	AX713379 Sequence 63 AX713379			Isogai,T., Sugiyama,T., Otsuki,T., Wakamatsu,A., S. Yamamoto,J.I., Isono,Y., Hio,Y., Otsuka,K., Nagai, Tamachika T. Soki N. Vochikada T. Otsuka N. Nay	Masuho, Y. Pill-length CDNAs Darat. Ep 1002660, 62 10 NAB-2000.		<pre>ie 1. 2094 /organism="Homo sapiens" /mol_type="unassigned bNA" /db_xref="taxon:9606"</pre>		Query Match 67.4%; Score 855.6; DB 6; Length Best Local Similarity 81.5%; Pred. No. 8.3e-168; Matches 1095; Conservative 0; Mismatches 174; Indels	1 ATGGCTGCAGCTAGCGTGACCCCCCTGGCTCCCTGGAGTTGCTACAGCCCGGCTTCTCC	61 AAGACCTTCTGGGGACCAAGTGGAAGCCAAGTACTGTGGTCCGCTGCAGAAAGGTCTTGTAGTTCTGCTCGCTGCAGAAACGTCTAGAAAACGTCAAGAAAAAAAA	121 CTCCCCAGGCCCTTCCAGGCCAGTGCTGCCAGTACTGCTCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGC	181 ATCCTCAGCTCTGGGCCTCAGAACTGTGCTGCCTGTCTCACGAGGGCATATATGAAGAA 	241 GGCATTICTATITIAGAAAGCAGITCGGCCTTCCCAGALAAIGCTGCCGCAGGGAGGIG 	301 GAGAGCCTGCCGGCCGTCTGTCCCAGTGATGGATGCACCTGGAAGGGGACCCTGAAAGAA
d Q H		č qq	RESULT 14	AX713379 LOCUS DEFINITION ACCESSION	VERSION KEYWORDS SOURCE	OKGANISM	KEFEKENCE AUTHORS	TITLE	FEATURES	source	ORIGIN	Query M Best Lo Matches	Qy Dp		8 & 8	S G	DP OA	<i>8</i>

1125

Homo sapiens

ORGANISM

REFERENCE AUTHORS

AK054686

ACCESSION VERSION KEYWORDS SOURCE

LOCUS

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LPAVCPSDGCTWKGTLKEYEVKMPACGMVTEAPAVGSRPRSPSSYDLVLHVPLTGAEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RAPCCGADVKAHHEVCPKFPLTCDGCGKKKIPREKFQDQDKIBALSSKVQQLERSIGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       345 GAGAGCCTGCCGGCCGTCTGTCCCAGTGATGCATGCACCTGGAAGGGACCCTGAAAGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 1095; Conservative
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AKO54686 2094 bp mRNA linear PRI 30-JAN-2004 Homo sapiens cDNA FLJ30124 fis, clone BRACE1000093, highly similar to TNF RECEPTOR ASSOCIATED FACTOR 2.
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Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Wakamatsu,A., Ishi,S.,
Yamamoro,J., Isono,Y., Kawai-Hio,Y., Satio,K., Nishikawa,T.,
Kimura,K., Yamashita,H., Matsuo,K., Nakamura Y., Sakine,M.,
Kikuchi,H., Kanda,K., Wagatsuma,M., Murakawa,K., Kanehori,K.,
Takahashi-Fujii,A., Oshima,A., Sugiyama,A., Kawakami,B.,
Sugano,S., Magahari,K., Masuho,Y., Nagai,K. and Isogai,T.
Unpublished
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                          AKO54686.1 GI:16549280
oligo capping; fis (full insert sequence)
Homo sapiens (human)
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/mol_type="mRNA"
/db_xref="taxon:9606"
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human cDNAs

PUBMED REFERENCE

JOURNAL

TITLE

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300 344 360 409 464 429 524 484

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Source

PEATURES

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946 TACCTGAACGGCAACGGCACCGCGACGAACACCTGTCCCTCTTTGTGGTGATG 1005

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765 TGTGACGGCTGCGGCAAGAAGATCCCCCGGGAGAAGTTTCAGGACCAAGACAAGATT 824

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Aad01947 Human TRA	Acf04633 TRAF2 pro	Adm45823 TNF-alpha Aaa55491 Himan TRA		Lund		Acd13346 Human DNA	Adb80997 RING-SH C	Ada52495 Human cod	Abi99821 Mouse isc	Aat12262 Mouse TRA	Aca57328 Human adi	Aat31274 Epstein-B	Aaa55490 Human TRA		5 Novel	Abx63823 Human cDN	ഹ	Adl82946 Human PRO
SUMMARIES	AAD01947 AAD01948	ACF04633	ADM45823 AAA55491	AAD01949	ABL65876	ABL67670	ACD13346	ADB80997	ADA52495	ABI99821	AAT12262	ACA57328	AAT31274	AAA55490	ABK84255	ADF76475	ABX63823	ADL22895	ADL82946
DB	l w w	10	3 1	'n	9	9	ω	σ	10	9	N	œ	71	m	9	10	ω	12	12
Length	2025	1506	1506	2262	2262	2262	2262	2262	2094	2121	2121	979	2380	2380	2380	2380	5981	2412	2412
% Query Match	100.0	75.6	75.6	75.6	75.6	75.6	75.6		67.4	55.2	55.1	45.9	23.4	23.4	23.4	23.4	23.4	23.2	23.2
Score	1269	929.6	9 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	928.6	9:636	9:636	926.6	929.6	855.6	701	699.4	582.2	296.6	296.6	296.6	296.6	296.6	295	σ
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Ado19523 Human PRO	Ado20498 Human PRO	Aaa39476 Human TNF	574 Human	642	Ach41674 Human foe	Aat12261 Mouse TRA	. Aak83299 Human imm	Aca90241 INF-recep	Abn85403 Human NOV	Aca90242 INF-recep	5397	Abl68936 Kidney ca	3881	DNA e	Abt08314 Human NOV	_	Aat88023 Human TRA	4	Adb80986 RING-SH c	Adl22894 Human MP2	Aat88022 Murine TR	Aat87039 DNA encod	Aal46792 Murine CD
AD01952		AAA39476	AAD63574	ADG47642	ACH41674	AAT12261	AAK83299	ACA90241	ABN85403	ACA90242	ABN85397	ABL68936	ACA89881	AAT87040	ABT08314	331	AAT88023	AAA55494	_	ADL22894	302	AAT87039	AAL46792
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22	23	24	25	56	c 27	28	c 59	30	31	32	33	34	35	36	37	38	39		41	42	43	44	45

ALIGNMENTS

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Human; tumour necrosis factor; TNF; TRAF2-FL; inhibitor; treatment; TNF-receptor associated factor; TRAF2 truncated; TRAF2TR; antinflammancry; cardiant; myocardial infarction; splice variant; vasotropic; antipsoriatic; antirheumatic; antiarthritic; antidabetic; antiarteriosclerotic; immunosuppressive; Crohn's disease; psoriasis; rheumatoid arthritis; graft versus solve disease; cardiovascular disease; non-insulin dependent diabetes; inflammatory bowel disease; stroke;
                                                                                                                                                                                                                                                                                                              Location/Qualifiers
55. 1323
/*tag=
/product= "TRAF2TR protein"
/note= "This region is specifically claimed in claim 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acid encoding variants of tumor necrosis factor receptor associated factors useful for inhibiting tumor necrosis factor alpha-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clark KL;
                                                                                                                     Human TRAF2 splice variant TRAF2TR (TRAF2 truncated) cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Guo K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Searfoss GH, Pagnoni MF, Ivashchenko YD,
                              AAD01947 standard; cDNA; 2025 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (AVET ) AVENTIS PHARM PROD INC.
                                                                                                                                                                                                                                                          neurodegenerative disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-APR-2000; 2000WO-US009178.
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                                                                                        (first entry)
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P-PSDB; AAY71901.
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                                                          AAD01947;
RESULT 1
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us-10-018-030b-1.rng

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(first entry)
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                                                                              receptor associated factor truncated protein (TRAP2TR) which is a splice variant of human TRAP2 protein. TRAP2TR has an ability to inhibit TMP alpha signalling pathways. The TRAP2TR variant is useful for inhibit TMP diseases involving hyperactivation of TWI TRAP2TR variant is useful for inhibiting involving hyperactivation of muclear factor kappa B (NFRB). The variant is also useful for inhibiting and treating inflammatory processes involving TWPalpha such as Crohn's disease, psoriasis, rheumatoid arthlists, graft versus host disease, non-insulin dependent diabetes, inflammatory bowel disease, and neurodegenerative diseases or cardiovascular disease such as cardiac ischaemia-reperfusion injury (collowing myocardial infarction, coronary artery bypass surgery, cardiac transplantation or ischaemia-reperfusion injury in the central nervous system (CNS) following stroke, the progression and rupture of advanced congestive heart failure, endothalial cell injury following balloon angioplasty, or apoptotic cell death of myocardial cells
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                                                                      present sequence is a cDNA encoding tumour necrosis factor (TNF)-
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regulated pathways, and for treating Crohn's disease, psoriasis, and rheumatoid arthritis.
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                                           Claim 1; Fig 4a; 74pp; English.
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Matches 1269, Conserv
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TNF-receptor associated factor; TRAF2 truncated-daleted; TRAF2TD;
antinflammatory; cardiant; mutant; mutein; myccardial infarction;
vasotropic; antipsoriatic; antiheumatic; antiarthritic; antidiabetic;
antiarteriosclerotic; immunosuppressive, Crohn's disease; psoriasis;
rheumatoid arthritis; graft versus host disease; cardiovascular disease;
non-insulin dependent diabetes; inflammatory bowel disease; stroke;
                                   GCCGAGGCCTGCAGCCGGCGGCAGCACCGGCTGGACCAAGACTGAAGCCCTGAGTAGC
                                                                                                                                               AAGGTGCAGCTGGAGAGGAGCATTGGCCTCAAGGACCTGGCGATGGCTGACTTGGAG
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GCCGAGGCCTGCAGCCGCCAGCACCGCTGGACCAAGATTGAAGCCCTGAGTAGC
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/*tag= a
/product= "TRAF2TD protein"
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CACCGGCTGGACCAAGACAAGATTGAAGCCCTGAGTAGGAGGAGGTGCAGCAGCTGGAGAGG 483
364 TGCGTCCTGAACCGGGAGGTGGAGAGGGTGGCCATGACTGCCGAGGCCTGCAGCCGGCAG 423
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                                                                                                                                            <u> AGCATTGGCCTCAAGGACCTGGCGATGGCTGACTTGGAGCAGAAGGTCTTGGAGATGGAG</u>
                                                                                                                                                                             AGCATTGGCCTCAAGGACCTGGCGATGCCTGAACTTGGAAGGTCTTGGAGATGTGGAGA
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receptor associated factor truncated-deleted (TRAF2TD) protein which is a
variant of human TRAF2TR (truncated). This sequence includes both the
naturally occurring splice variation and a deletion at the 5' end of
human TRAF2-FI (full-length) nucleic acid sequence. TRAF2TD has an
ability to inhibit TNF alpha signalling pathways. THE TRAF2TD variant is
useful for inhibiting diseases involving over production of TNFalpha,
TNFalpha pathologies involving Hyperactivation of muclear factor kappa B
(NFRB). The variant is also useful for inhibiting and treating
TNFalpha pathologies involving TNFalpha such as Crohn's disease,
CHAPB). The variant is also useful for inhibiting and treating
CHAPB). The variant dashes involving TNFalpha such as Crohn's disease,
Described a cardiovascular disease such as cardiac ischaemia-reperfusion
injury following myocardial infarction, coronary artery bypass surgery,
cardiac transplantation or ischaemia-reperfusion injury in the central
nervous system (CNS) following stroke, the progression and rupture of
congestive heart failure, endothelial cell injury following balloon
congestive heart failure, endothelial cell injury following balloon
cardiovardial cell death of myocardial cells
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Matches 1008; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to a purified complex comprising a lymphotoxin beta receptor (LTbetaR) polypeptide and Smac polypeptide. The lymphotoxin-beta receptor (LTbetaR) complex is useful for identifying modulators of LTbetaR activity or expression for treating or preventing cancer or an immune disorder such as autoimmune disorder, e.g. rheumatoid arthitis, systemic lupus erythematosus, Goodpasture's syndrome, Grave's disease, Hashimoto's thyroiditis, pemphigus vulgaris, myasthemia gravis, scleroderma, autoimmune haemolytic anaemia, autoimmune thrombocytopenic purpura, polymyositis, dermatomyositis, pernicious anaemia, Slogren's syndrome, ankylosing spondylitis, vasculitis, or type I diabetes mellitus. The present sequence is the coding sequence of a TRAF2 protein, which forms part of the complex of the invention
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Pred. No. 1.7e-205;
0; Mismatches 39; Indels 237;
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Best Local Similarity 81.7%;
Matches 1230; Conservative
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                                                                                                       Wooters JL,
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                                                                                                             protein complex; tumour necrosis factor alpha receptor; TNF-alpha; TNI nuclear factor; NF-*AppaB activating kinase; NAK; RasGAPB; Lransducin repeat-containing protein; TRCP1; TRCP2; antiinflammatcry; cytostatic; inflammation; apoptosis; gene therapy; ss; gene; TRAF2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to antisense oligonucleotides (see AAA55496 - A5557) which are targeted to nucleic acids encoding a human tumour necrosis factor receptor-associated factor (TRAF). The antisense requences comprise at least one modified internucleotide linkage, which is a phosphorothicate linkage. The oligonucleotides also include at least one modified super moiety such as a 2-O-methoxyethyl sugar moiety. Sequences AAA55496-A55495 represent nucleotide sequences encoding human TRAF1-6. Included in the invention is a method for treating a human having a disease associated with the expression of TRAF comprising administering an antisense oligonucleotide. The reduction of jun kinase activation in cells comprises contacting the cells with an antisense oligonucleotide targeted to TRAF-6. The selectin expression in cells or TRAF-6. The method for the reduction of F selectin expression in cells or TRAF-6. The method for the reduction of F selectin expression in cells or TRAF-6. The method for the reduction of F selectin expression in cells or tissues comprises contacting the cells or tissues with an antisense oligonucleotide have antiproliferative and anti-first inflammatory activity and are useful for treating disorders associated with cell proliferation and inflammation. The antisense oligonucleotides have antiproliferative selectines.
                                                                                             AAGAATTCCTACGTGCGGACGAIGCCATCTTCATCAAGGCCATTGIGGACCTGACAGGG 1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antisense oligonucleotides targeted to nucleic acids encoding human tumor necrosis factor receptor-associated factor (TRAF), useful for treating diseases associated with TRAF expression such as inflammatory diseases.
AACGACATGAACATCGCAAGCGGCTGCCCCCTTCTTCTGCCCCGTCTCCCAAGATGGAGGCA
                         AACGACATGAACATCGCAAGCGGCTGCCCCTCTTCTGCCCCGTCTCCAAGATGGAGGCA
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                                                                                                    Areacracaacracacccccragcrccrasaarracracacccaacrrcrc
                      Gaps
                      Indels 237;
  Pred. No. 1.9e-205;
0; Mismatches 39;
81.7%;
  Best Local Similarity 81.7
Matches 1230; Conservative
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1075 AAGGTCAGGCCCTICCAGGCGCAGTGTGGCCACCGGTACTGCTCCTTCTGCCTGGCCAGC 1134
                                                                                                                                                                                                                                                                                                                                                                                                                   1495 AAGAATTCCTACGTGCGGGACGATGCCATCTTCATCAAGGCCATTGTGGACCTGACAGGG 1554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; tumour necrosis factor; TNP; TRAF2; inhibitor; treatment;
TNF-receptor associated factor; TRAF2 truncated; TRAF2TR;
TRAF2 truncated deleted; TRAF2TD; antiinflammatory; cardiant; vasotropic; antipsoriatic; antirhematic; antiarthritic; antidiabetic; antimensembers antiarteriosclerotic; immunosuppressive; Crohn's disease; psoriasis; rheumatoid arthritis; graft versus host disease; cardiovascular disease; non-insulin dependent diabetes; inflammatory bowel disease; stroke;
                                                                                                                                                                                                                                                                                           GAGCACGTGATTGACGCCTTCAGGCCCGACGTGACTTCATCTCTTTTCAGAGGCCAGTC
                                               1195 TTCTACACCAGCAGGTACGGCTACAAGATGTGTGTGCGTATCTACCTGAACGGCGACGGC
                                                                                                                                                                                                                                    1315 CTGCTGCGGTGGCCCTTCAACCAGAAGGTGACCTTAATGCTGCTCGACCAGAATAACCGG
                                                                                                                                                                                                                                                                  1084 GAGCACGTGATTGACGCCTTCAGGCCCGACGTGACTTCATCCTCTTTTCAGAGGCCAGTC
                                                                                                                                                                                                                                                                                                                                                         AACGACATGAACATCGCAAGCGGCTGCCCCTCTTCTGCCCCGTCTCCAAGATGGAGGCA
                            844 TTCGCCAGGAAGCTCCAGGAAGCTGTGGCTGGCCGCATACCCGCCATCTTCTCCCCCAGCC
                                                                                      TICTACACCAGCAGGIACGGCTACAAGAIGTGTGTGTGTGTGTATCTACCTGAACGGCGACGGC
                                                                                                                                                                                                          CTGCTGCGGTGGCCCTTCAACCAGAAGGTGACCTTAATGCTGCTCGACCAGAATAACCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= c
/note= "This region is truncated both in TRAF2TR and
TRAF2TD nucleic acid sequences"
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The present sequence is a cDNA encoding a full-length (i.e. non-spliced)

[Corm of human tumour necrosis factor (TNF)-receptor associated factor

[TRAF2] procein (referred to in the specification as TRAF2-FL. TRAF2-FL

has two variants, a splice variant of TRAF2 referred as "TRAF2 runcated"

[Corm of arther than a TRAF2 expression construct with enhanced dominant

[Corm of arther trafact of the specification of TRAF2-TD.

[Corm of TRAF2-TD are capable of inhibiting TNF alpha signalling

[Corm of the trafact of trafact of inhibiting diseases involving

[Corm of nuclear factor kappa B (NFRB). The variants are also

[Corm of nuclear factor kappa B (NFRB). The variants are also

[Corm of nuclear factor kappa B (NFRB). The variants are also

[Corm of nuclear factor kappa B (NFRB). The variants are also

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[Corm of nuclear factor kappa B (NFRB). The variants are also

[Corm of nuclear factor f
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                                                                                                                                                                                                                                                                          New nucleic acid encoding variants of tumor necrosis factor receptor associated factors useful for inhibiting tumor necrosis factor alpharegulated pathways, and for treating Crohn's disease, psoriasis, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels 237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 2262;
                                                                                                                                                 Clark KL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2262 BP; 452 A; 664 C; 727 G; 419 T; 0 U; 0 Other;
                                                                                                                                                    Guo K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 959.6; DB 5;
Pred. No. 1.9e-205;
0; Mismatches 39;
                                                                                                                                                    Ivashchenko YD,
                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; Fig 4a; 74pp; English.
                                                                                                   (AVET ) AVENTIS PHARM PROD INC
                                                   99US-0131940P.
06-APR-2000; 2000WO-US009178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         75.6%;
llarity 81.7%;
Conservative
                                                                                                                                                    Pagnoni MF,
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                                                                                                                                                                                                                                                                                                                                                           rheumatoid arthritis
                                                                                                                                                                                                 WPI; 2001-007223/01.
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Best Local Similarity
Matches 1230; Conserv
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stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
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Horrigan S;

us-10-018-030b-1.rng

The present invention describes a method (M1) for screening for an antineoplastic agent. The method involves exposing cells to a chemical agent to be tested for antineoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 8447 sequences (given in Ab161664 to Ab170110), or is at least 954 identical to (S), where a change in extivity and can be used in gene therapy. M1 can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of M1, and the data is sufficient to convey the chemical structure and/or properties of the agent. M1 can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidhey, prostate or pancreatic cancer, adenous cancer, infiltrating lobular cancer, squamous call carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set. Ebner R, Endress G, Claim 1; SEQ ID NO 4213; 44pp; English Carter KC, Augustus M, Weaver Z; WPI; 2002-188264/24 Young PE, Soppet DR,

Sequence 2262 BP; 452 A; 664 C; 727 G; 419 T; 0 U; 0 Other;

120 240 300 354 360 414 364 364 534 364 55 ATGGCTGCAGCTAGCGTGACCCCCCCTGGCTCCCTGGAGTTGCTACACCCCGGCTTCTCC 114 174 CTCCGCAGGCCCTTCCAGGCGCAGTGTGGCCACCGGTACTGCTCCTTCTGCCTGGCCAGC 180 234 294 415 TACGAGAGCTGCCACGAAGGCCGCTGCCCGCTCATGCTGACCGAATGTCCCGGCGTGTAAA 474 594 ----- 364 9 AGACCCCCCCCGGGGACCAAGCTGGAAGCCAAGTACCTGTGCTCCGCCTGCAGAAACGTC GAGAGCCTGCCGGCCGTCTGTCCCAGTGATGCACCTGGAAGGGGACCCTGAAAGAA AAGACCCTCCTGGGGACCAAGCTGGAAGCCAAGTACCTGTGCTCCGCCTGCAGAAACGTC ATCCTCAGCTCTGGGGCCTCAGAACTGTGCTGCCTGTGTTCACGAGGGCATATATGAAGAA Arcercagereregecercagaacreregecergrerreacagegearararaaaaa 295 GGCATTTCTATTTTAGAAAGCAGTTCGGCCTTCCCAGATAATGCTGCCCGCAGGGAGGTG GAGAGCCTGCCGGCCGTCTGTCCCAGTGATGCACCTGGAAGGGGACCCTGAAAGAA 475 GGCCTGGTCCGCCTTGGTGAAAAGGAGCGCCACCTGGAGCACGAGGTGCCCGGAGAAGC 535 CTGAGCTGCCGGCATTGCCGGGCACCCTGCTGCGGAGCAGAGGTGAAGGCGCACACGAG GGCATTTCTATTTTAGAAAGCAGTTCGGCCTTCCCAGATAATGCTGCCCGCAGGGAGGTG ATGGCTGCAGCTAGCGTGACCCCCCCTGGCTCCCTGGAGTTGCTACAGCCCGGCTTCTCC credecadecerrecadeceadatadeceacederacrecrecrrecerdecade Gaps Score 959.6; DB 6; Length 2262; Pred. No. 1.9e-205; 0; Mismatches 39; Indels 237; Query Match Best Local Similarity 81.7%; Matches 1230; Conservative TACG 115 235 355 361 365 61 121 175 181 241 301 365 365 g ò g ò D ò ద 8 ద ò g $\dot{\circ}$ 셤 δ à d δ g

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	424 ATCGGCTGCCTCGAGACGGTAGAGGGTGAGAACAGCAGGAGCACGAGGTGCAGGGGGGGG	4 (
	84 CGGGAGCCCGGCCCCCCCCTTGGGGGGAGCCCCCCTTGGGAGCCCCCCTTGGGAGAGCCCCTTTGGGAGAAGCCCCTTTGGGAGAAGCCCCTTTGGAAGAAGCCCTTTTGGAAGAAGCCCTTTTGAAGAAGCCCTTTTGAAGAAGCCCTTTTGAAGAAGCCCTTTTGAAGAAGCCCTTTTTGAAGAAGCCCTTTTTGAAGAAGCCCTTTTTTTT	5.
qq	GGGAGCACCTGGCCATGCTACTGAGCTCGGTGCTGGAGGCAAAGCCCCTTTGG	834
	544 CAGAGCCACGCGGGGTCAGAGCTCCTGCAGAGGTGCCAGAGCCTGGAGAAGAAGACGGCCCCCCCAGAAGAAGAAGAAGAAGAA	603
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δ	4 TTCGCCAGGAAGCTCCAGGAAGCTGTGGCCTGGCCGCATACC	903
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	904 TICTACACCAGCAGGTACGCTACAAGATGTGTCTGCGTATCTACTGAACGCGACGCC 	963
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Db 1	1255 ACCGGGCGAGGAACACACCTGTCCTTCTTTGTGGTGATGAAGGGCCCGAATGACGCC	1314
2y 1	1024 CTGCTGCGGTGGCCCTTCAACCAGAAGGTGACCTTAATGCTGCTCGACCAGAATAACCGG	1083
2,	84 GAGGACGTGATTGACGCCTTCAGGCCCGACGACGTCATCC	1143
Db 1	1375 GAGCACGTGATTGACGCCTTCAGGCCCGACGTGACTTCATCCTCTTTTTCAGAGGCCCAGTC	1434
2y 1	BACATCGCAAGGGCTGCCCCTTTCTGCCCCGTCT	1203
Db. 1	35 AACGACATGAACATCGCAAGCGCTGCCCCCTCTTCTGCCCCGTCTCCAAGAT	1494
2y 1	1204 AAGAATTCCTACGTGCGGGACGATGCCATCTTCATCAAGGCCATTGTGGACGACGAGG	12
Db 1	95 AAGAATTCCTACGTGCGGGACGATGCCATCTTCATCAAGGCCATTGTGGGACCTGACAGG	1554
Oy 1	1264 CTCTAA 1269 	
Db 1	SS CTCTAA 156	
RESULT 8 ABL67670 ID ABL67 XX	7670 standard; DNA; 2262 BP.	
ABL6	7670;	

the present invention describes as well as the control of the cont

tumour

present invention describes a method (MI) for screening for an anti-lastic agent. The method involves exposing cells to a chemical agent

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Augustus M,
                                                                                    (AVAL-) AVALON PHARM
                                                                                           WPI; 2002-188264/24.
               WO200194629-A2
            Homo sapiens,
                                                                                       Young PE,
Soppet DR,
          gene; ds.
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Human, cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
                                                       Oesophagus cancer related gene sequence SEQ ID NO:6007.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-JUN-2000; 2000US-0209473P.
18-SEP-2000; 2000US-0233617P.
18-SEP-2000; 2000US-0233617P.
20-SEP-2000; 2000US-0233617P.
20-SEP-2000; 2000US-0234003P.
20-SEP-2000; 2000US-0234003P.
22-SEP-2000; 2000US-0234924P.
22-SEP-2000; 2000US-0234924P.
25-SEP-2000; 2000US-0235634P.
25-SEP-2000; 2000US-0235634P.
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25-SEP-2000; 2000US-0235634P.
25-SEP-2000; 2000US-0235634P.
26-SEP-2000; 2000US-0235634P.
27-SEP-2000; 2000US-0235634P.
27-SEP-2000; 2000US-0235634P.
28-SEP-2000; 2000US-0236034P.
28-SEP-2000; 2000US-0236034P.
28-SEP-2000; 2000US-0236034P.
28-SEP-2000; 2000US-0236034P.
29-SEP-2000; 2000US-0236034P.
29-SEP-2000; 2000US-0236034P.
29-SEP-2000; 2000US-0236034P.
29-SEP-2000; 2000US-0236034P.
20-CCT-2000; 2000US-0237594P.
03-CCT-2000; 2000US-0237598P.
03-CCT-2000; 2000US-0237508P.
03-CCT-2000; 2000US-0237508P.
03-CCT-2000; 2000US-0237608P.
01-NOV-2000; 2000US-0237608P.
(first entry)
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                                                                                                                                                                                                                                                           Sequence 2262 BP; 452 A; 664 C; 727 G; 419 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 1230; Conserv
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484 CGGGAGCACCTGGCCATGCTACTGAGCTCGGTGCTGGAGGCAAAGCCCCTCTTGGGAGAC 543

Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set.

Claim 1; SEQ ID NO 6007; 44pp; English.

Horrigan

Endress G,

Ebner R,

Carter KC,

Funke

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ŗ Ħ,

Francis-Lang

Belvin M,

g 9

Plowman

Friedman L,

WPI; 2003-156859/15.

P-PSDB; ABC07170

EXEL-) EXELIXIS INC

05-JUN-2001; 2001US-0296076P. 10-OCT-2001; 2001US-0328605P. 15-FEB-2002; 2002US-0357253P. 03-JUN-2002; 2002WO-US017382

Identifying modulators of the p53 pathway for use in treating apoplor cell proliferation disorders, comprises screening for agents this modulate activity of a human ortholog of genes that modify the p53

Example 2; Page 180-181; 678pp; English

pathway in Drosophila.

WO200299122-A1.

12-DEC-2002

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The invention relates to identifying (M1) a candidate p53 pathway

C modulating agent, by contacting an assay system comprising a purified HM

CD polypeptide (human orthologue of genes that modify the p53 pathway in no prosophila) or nucleic acid with a test agent under conditions, where but brosophila or nucleic acid with a test agent under conditions, where but c activity, and detecting a test agent, the system provides a reference of the test agent, the system provides a reference c activity, and detecting a test agent-biased activity of the assay system.

CC activity, and actecting a test agent-biased activity of the assay system.

Also included are modulating (M2) a p53 pathway of a cell (comprising contacting a cell defective in p53 function with a candidate modulator contacting a cell defective in p63 function is restored), modulating (M3) a p53 pathway in a mammalian cell (comprising contacting the cell with an agent that specifically binds an HM polypeptide or nucleic acid) and diagnosing (M4) a disease in a patient (comprising; (a) obtaining a biological sample contacting the sample with a probe for HM expression contents and the results with a control; and (d) determining whether the comparison indicates a likelihood disease). (M1) is useful for identified by (M1) are useful in a variety of diagnosing breast, colon, kidney, lung and ovarian cancer, therapeutic applications, where disease or disorder prognosis is related to defects in the p53 pathway, such as, anglogenesis, apoptotic or cell proliferation of the cell, so that the cell undergoes normal contents appsible to the cell, so that the cell undergoes normal contents application or progression through the cell undergoes normal contents appetute acid encoding a p53 pathway of a cell, thus restoring the p53 pathway such as anglogenic or cell proliferation disorders. The present sequence is an HM concleic acid encoding a p53 pathway modifying protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 ATCCTCAGCTCTGGGCCTCAGAACTGTGCTGCTGTGTTCACGAGGGCATATATGAAGAA 240
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81.7%; Pred. No. 1.9e-205;
iive 0; Mismatches 39; Indels 237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2262 BP; 452 A; 664 C; 727 G; 419 T; 0 U; 0 Other;
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Human; ss; gene; p53 modifier; cytostatic; cancer; cytostatic; antiangiogenic; antiapoptotic; p53 pathway; breast cancer; colon cancer; kidney cancer; lung cancer; ovarian cancer; angiogenesis; cell cycle; apoptotic disorder; cell proliferation disorder.

Homo sapiens

Human DNA encoding a p53 modifier, SEQ ID 15.

(first entry)

13-AUG-2003

ACD13346;

ACD13346 standard; cDNA; 2262

235 MUTCHOROUTH THAT ANAMORE CONTROLLED TO THE C	1315 CTGCTGCGGTGGCCCTTCAACCAGAAGGTGACCTTAATGCTGCTCGACCAG	1084 GAGCACGTGAT 1375 GAGCACGTGAT	1144 AACGACATGAACATCGCAAGCGGCTGCCCCTCTTCTGCCCCGTCTCCAAG	1204 AAGAATTCCTACGTGCGGGACGATGCCATCTTCATCAAGGCCATTGTGGAC	1264 CTCTAA 126	1555	3ULT 10 380997		ADB8099/; 04-DEC-2003 (first entry)		RING-SH 3; Gag protein; Gag late domain; PI3K; actin; myosin Hsp70; Hsp90; STAM1; STAM2A; STAM2B; VHS-UIM; GTPase; E2 enz: cullin; RING-SH; clathrin; virucide; vaccine; antiviral; ret:		Unidentiled. W02003033646-A2.	24-APR-2003.	31-JUL-2002; 2002WO-US024589.	31-JUL-2001; 2001US-0308958P. 09-NOV-2001; 2001US-0345846P.	(PROT-) PROTEOLOGICS INC.	Greener T, Moskowitz H, Reiss Y, Alroy I;	WPI; 2003-393509/37. P-PSDB; ADB80956.		and for treating viral disorders caused by or filoviruses.					identifying agents having antiviral activity, and for treatification disorders caused by retroviruses, rhabdoviruses, or filovirus polynucleotide represents a DNA sequence relating to a proteithe RIMG-SH complex of the invention		
214 GEOLITICALITITICALITA CANAGONITICA CONTRIBUTION	ä	6 B	<i>6</i> គ	៩ គ	8	ដ	R	# 2 ;	3 2 5	252	222	ž X (388	X E	XFX	8 8 8	X &	XI	3	XEE	E E X	S X	1888	888	3888	3885	3 X 8	
214 GEOLITICALITITICALITA CANAGONITICA CONTRIBUTION									***************************************												·							- ,
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novel isolated protein complex comprising a polypeptide selected from a Gag protein, a n, myosin, Hsp60, Hsp90, STAMI, STAMISA, an E2 enzyme, tsg101, a cullin, RING-SH, and a complex has virucide activity and can be used of a vaccine. The protein complex and detecting cells infected with a virus, for ntiviral activity, and for treating viral ntiviral activity, and for treating viral ruses, rhabdoviruses, or filoviruses. This DNA sequence relating to a protein comprising invention.
                                             CGGCTGCCCCCTTTCTGCCCCGTCTCCAAGATGGAGGCA 1203
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CCAGAAGGTGACCTTAATGCTGCTCGACCAGAATAACCGG 1374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ate domain; P13K; actin; myosin; Hsp60;
STAM2B; VHS-UIM; GTPase; E2 enzyme; tsg101;
ds;
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New polynucleotides encoding full-length polypeptides, e.g. secretory and/or membrane proteins, useful for developing medicines for diseases in
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R, Tamechika
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                                                     ATCCTCAGGAAGCTCCAGGAAGCTGTGGCTGGCCGCATACCGGCCATCTTCTCCCCAGCC
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pai K, Irie F
Masuho Y;
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Hio Y, Otsuka K, Nagai
Otsuka M, Nagahari K, N
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24-JAN-2002; 2002US-0350435P.
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Yoshikawa T,
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P-PSDB; ADA54134.
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                                                 ATGGCTGCAGCTAGCGTGACCCCCCTGGCTCCCTGGAGTTGCTACAGCCCGGCTTCTCC
                           Gaps
                          237;
  Length
                          Indels
  Score 959.6; DB 9;
Pred. No. 1.9e-205;
0; Mismatches 39;
  Query Match 75.6%;
Best Local Similarity 81.7%;
Matches 1230; Conservative
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                                                                         GCCATCTTCTCCCCCAGCCTTCTACACCAGCAGGTACGGCTACAAGATGTGTCTGCGTATC
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 or as target molecules for gene therapy
                                                              The present invention relates to novel human secretory or membrane proteins (ADA54072-ADA55710) and their coding sequences (ADA52433-ADA54071). The coding sequences are useful in the gene therapy of diseases caused by abnormalities of the proteins, e.g. cancer, inflammatory diseases, osteoporosis or neurological disease.
                                                                                                                                                                                                   67.4%; Score 855.6; DB 10; Length 2094; ilarity 81.5%; Pred. No. 4.1e-182; Conservative 0; Mismatches 174; Indels 75;
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The present invention describes a method for examining ischaemic conditions, comprising measuring the expression levels of particular genes (1) in a test sample odetermining the expression profile of a gene group in the sample comprising genes selected from (T). The method is useful for examining the ischaemic condition (e.g. compressive ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring expression levels of particular genes (AB199202 to AB19912, encoding the protein sequences in ABB57020 to ABB57374) or by determining the expression profile of a gene group comprising these genes. The expression lindicator when screening for ischaemic condition. Improving drugs or therapeutics for ischaemic diseases. AB199913 and AB199914 represent PCR primers for a mouse ischaemic ondition related sequence, which are used in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                   A cDNA clone (AAT12262) coding for tumour necrosis factor receptor associated factor 2 (TRAF2) (AAR90578) was isolated using a yeast two-hybrid system to assay for proteins that associate with the intracellular domain (ID) of tumour necrosis factor receptor type 2 (TNF-R2). The cDNA is used for produ. of recombinant TRAF2, a new factor capable of specific association with TNF-R2 ID and CD40
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                                                                                                                                                                                                                                Tumour necrosis factor (TNF) receptor-associated factors - involved in mediation of biological activities of TNF and CD40 ligands.
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                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2121 BP; 506 A; 560 C; 616 G; 439 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                        Example 3; Page 73-74; 116pp; English
                                                                   94US-00250858.
94US-00331394.
95US-00446915.
                                            95WO-US006639
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P-PSDB; AAR90578.
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28-OCT-1994;
22-MAY-1995;
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               07-DEC-1995
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The invention relates to a complex between two interacting proteins in adipocyte cells, given in the specification. The proteins are identified by selecting a bait protein from a known adipocyte marker and then performing a past 2-hybrid selection to isolate prey proteins encoded by members of an adipocyte cDNA library. The proteins are designated SID (RTM) (selected interacting domains) proteins. Also included are a polymorlectide encoding a polypeptide in the adipocyte cells, a combinant host cell expressing at least one of the interacting polypeptides of the comprising any of the 738 amino acid sequences given in the specification (including its fragment or variant), a solution in the specification (including its fragment or variant), a vector comprising the SID (RTM) polymorlectide, a recombinant host cell comprising the vector, a protein chip comprising the polypeptides, polymorlectides and compounds are useful for preventing or treating metabolic disorders such as obesity or diabetes. The complex, polymorlectides and compounds are useful for preventing or treating metabolic disorders such as obesity or diabetes. The polymorlectides and compounds are useful for particularly useful for identifying selected interacting domains (SID (RTM)) for screening drugs that medulate the protein interaction, thus contain the therapeutic effect. The present sequence encodes a SID (RTM) between the protein interaction, thus the propertion of the difference of the difference of the companion of the substituting the polymorlectides and compounds are useful for the therapeutic effect. The present sequence encodes a SID (RTM) that there are sequences are sections of the sequence and the sequence of the sequence and substituting the polymorlectides and the sequence and sequence and substituting the sequence and sequence and sequences are substitutions and sequences are settles that the sequences are 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New complex between two interacting proteins in adipocyte cells, useful for identifying selected interacting domains that modulate protein interactions, or for preventing or treating metabolic disorders such as obesity or diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ccessasaagrrrcassaccaasaccaasarrcaascccrsastrascaassaccass
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                                                              Human, 88; gene, prey, adipocyte, SID; selected interacting domain; anorectic; antidiabetic; protein-protein interaction; diabetes; yeast 2-hybrid assay; metabolic disorder; obesity.
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                    Human adipocyte Selected Interacting domain, SID, cDNA #415
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Pred. No. 7.8e-121;
0; Mismatches 8;
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ilarity 98.7%;
Conservative
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Best Local Similarity
Matches 587; Conserv
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                                                                                                                                                                                                                    WO200286122-A2
                                                                                                                                                                     Homo sapiens
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                                                                                                                                                                                          804
                                                                                                                                                                                                                                      684
                                                                                                                                                                                                                                                                                                     865 CATCGCAAGCGCCTCCTCCTCTCCCCCTCTCCAAGATGGAAGTTCCTA 924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Compounds and methods for controlling TRAF-mediated signals - by modulating interactions between Epstein Barr virus encoded proteins LMP1, LAP1, TNF, TNFR to inhibit lymphoblast growth and tumorigenesis.
                                                                         CAGGTACGCTACAAGATGTGTCTGCGTATCTACCTGAACGGCGACGGCACCGGCGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Epstein-Barr induced protein 6; LAP1; LMP1 associated protein 1;
                        565 GCGCCAGGÁAGCTGTGGCTGGCCGCATACCCGCCATCTTCTCCCCAGCCTTCTACACCAG
                                                                                                                           AACACACTGTCCCTCTTCTTGTGGTGATGAAGGCCCGAATGACGCCCTGCTGCTGCTG
                                                                                                                                                               GCCCTTCAACCAGAAGGTGACCTTAATGCTGCTCGACCAGAATAACCGGGAGCACGTGAT
                                                                                                                                                                                       745 GCCCTTCAACCAGAAGGTGACCTTAATGCTGCTCGACCAGAATAACCGGGAGCACGTGAT
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GCTCCAGGAAGCTGTGGCTGGCCGCATACCCGCCATCTTCTCCCCCAGCCTTCTACACCAG
                                                                                                                                                                                                                      TGACGCCTTCAGGCCCGACGTGACTTCATCCTCTTTTCAGAGGCCAGTCAACGACATGAA
                                                                                                                                                                                                                                                                                                                                 CGTGCGGGACGATGCCATCTTCATCAAGGCCATTGTGGACCTGACAGGGCTCTAA 1269
                                                                                                                                                                                                                                                                                                                                                 CGTGCGGGACGATGCCATCTTCATCAAGGCCATTGTGGACCTGACAGGGCTCTAA 979
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tumour necrosis factor receptor associated factor; TRAF;
signal transduction; TNF; TNFR; Jymphoblast; tumorigenesis; AIDS;
Hodgkin's disease; Burkitt's Jymphoma; naspharyngeal carcinoma;
mononucleosis; Epstein-Barr virus; EBV; gene therapy; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Epstein-Barr induced protein EBI6 gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; Page 61-63; 87pp; English
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76. .1326
/*tag= a
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                  A DNA sequence (AAT31274) codes for a novel B-cell protein (AAW03147) induced by Epstein-Barr virus (EBV) infection, termed Epstein-Barr induced protein 6 or EB16. The protein appears to be the human homologue of murine tumour necrosis factor receptor (TNFR) associated factor TRAF1. The gene can be used in gene therapy protocols for controlling TRAF-mediated TNFTNFR signal transduction, or for the prodn. of EB16 polypeptides that inhibit LMP1-TRAF interaction for use in treating infection and controlling cell growth/tumourigenesis associated with LMP1-encoding viruses, partic. EBV
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                                                                                                                                                                                                                                                                                                                              Score 296.6; DB 2; Length 2
Pred. No. 1.2e-56;
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Sequence 2, Application US/09167109

Batent No. 639297

GENERAL INFORMATION:

APPLICANT: Baker, Brenda F.

APPLICANT: Monia, Brett P.

APPLICANT: Monia, Brett P.

APPLICANT: Monia, Brett P.

TILE OF INVENTION: ANNISENSE MODULATION OF TRAF EXPRESSION
FILE REFERENCE: ISPH-0321

CURRENT APPLICATION NUMBER: US/09/167,109

CURRENT FILING DATE: 1998-10-06

NUMBER OF SEQ ID NOS: 228

SEQ ID NO 2
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llarity 81.7%; Pred. No. 1.5e-228;
Conservative 0; Mismatches 39;
ALIGNMENTS
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NAME/KEY: CDS
LOCATION: (156).
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: U12597 Genbank
DATABASE ENTRY DATE: 1996-02-16
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TYPE: DNA
ORGANISM: Homo sapiens
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Matches 1230; Conserv
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Sequence 2, 1
Sequence 1, 1
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/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                     GenCore version 5.1.6
Copyright (c),1993 - 2004 Compugen Ltd.
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	on US/08250858 1. David V. Mike Tumor Necrosis Factor Receptor-Ass Sis 62 Sis 62 Sis 62 Trancisco is Francisco is Prancisco is Pranc	Ouery Match Sole 701; DB 1; Length 2121; Best Local Similarity 71.0%; Pred: No. 2e-164; Matches 1068; Conservative 0; Mismatches 200; Indels 237; Gaps 1; Qy 1 ATGGCTGCAGCTGCAGCTCCCCCCTGGATTGCTACAGCCCGGCTTCTCC 60
181 ATCCTCAGCTCTGGGCCTCAGAACTGTGCTGTTCACGAGGGCATATATGAAGAA 240 228 ATCCTCAGCTCTGGGCCCCAGAACTGTGCTGTCTATGAAGAA 287 228 ATCCTCAGCTCTGGGCCCCCAGAACTGTGCTGTCTATGAAGGAA 287 241 GGCATTTCTATTTTAGAAAAGCAGTTCGGCCTTCCCAGATAATGCTGCCGCAGGAGGTG 300 288 GGCATTTCTATTTTAGAAGAGTTCGGCCTTTCCCAGATAACGCTGCCGCAGAGAGGTG 347 301 GAGAGCCTGCCGGCGTCTGTCCCAGTGATGGATGCACCTGGAAGAGAA 407 348 GAGAGCCTGCCGGCGTCTGTCCCAGTGATGGATGCACCTGGAAGGAGACCTGAAAGAA 407 361 TACGA 364 GAGAGCCTGCCGCAGTGTTGCCCATTCCTGCTGCAGGAGGGCCTTGAAAGAA 407 365	CTGAGCTGCCAGCACTGCAGAGCACCCTGTAGCCACTGGACCTGGAGGTACACTATGAG -GTTTCAGGACCACTGCAGAGCACCCTGTAGCCAGCAGCACCTGGAGGTACACTATGAGCACTGCCAGGAGTTCCAGGAGCTTCCAGGAGTTCCAGGAGTTCCAGGAGATTCTTCAGAGACTCCAGGAGCTTCCAGGAGATTCTTCAGAGACTCCAGGAGACTCCAGGAGACTCCAGGAGCTCCAGGAGCTCAGGAGACTCCAGGAGCTCCAGGAGACTCCAGGAGACTCCAGGAGACTCCAGGAGACTCCAGGAGACTCCAGGAGACTCCAGGAGACTCCAGGAGCTCCAGGAGACTCCAGGAGCTCCAGGAGACTCCAGGAGCTCCAGGAGACTCCAGGAGACTCCAGGAGACTCCAGGAGACTCCAGGAGACTCCAGGAGACTCCAGGAAGCTTCCAGGAACTCCCAGGAAACCTCCAGGAAGCTTCCAGGAACTCCCAGGAAACCTCCAGGAAACCTCCAGGAAACCTCCAGGAAACTCCCAGGAAACCTCCAGGAAACCTCCAGGAAACCTCCAGGAAACCTCCAGGAAACCTCCAGGAAACTCCCAGGAAACCTCCAGGAAACCTCCAGGAAACCTCCAGGAAACCTCCAGGAAACCTCCAGGAAACCTCCAGGAAACCTCCAGAAACCTCCAGAAAACCTCCAGAAAAAAAA	904 ITCTACACCAGGAGGACGCCTACAAGATGTGTTGCGTATCTACCTAACGAGGAGGGC 963 1188 ITCTACACCAGCAATATGGCTACAAGATGTGTTTACGAGGTCTACTTGAATGGCGACGGC 963 1188 ITCTACACAAGAATATGGCTACAAGATGTGTCTACGAGTCTACTTGAATGGCGACGGC 1247 964 ACCGGGCGAGGAACACACTGTCCTCTTTTTTGTGTGTGATGATGAGGCCCGAATGAGGCC 1023 1248 ACTGGGCGGGGAACATCTTGTTCTTTGTGTGTGATGAAGGCCCCAATGATGCT 1307 1024 CTGCTGCGGTGGCCCTTCAACCAGAAGGTCACCTTAATGCTGCTCGACCAGAATAACCGG 1083

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1488 AAGAATICCTATGTGCCGCGATGATGCCGATCTTCATCAAAGCTATTGTGGGACCTAACAGGA 1547
948 GAGGCTTGTAGCCGGCAGCACCGGCTAGACCAGGACAAGATTGAGGCCCTGAGTAACAAG 1007
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APPLICANT: Rothe. Mike
TITLE OF INVENTION: Tumor Necrosis Factor Receptor-Associated Factors
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
CONNTRY: USA
                                                                                 GTGCAGCAGCTGGAGGAGGAGTTGGCCTCAAGGACCTGGCGATGGCTGACTTGGAGGAG
                                                                                                                                                                                              AAGGICTIGGAGAAIGGAGCCAICCACCIACGAIGGGGICTICAICIGGAAGAICICAGAC
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/779,599
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CLASSIFCATION:
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: P0897C2
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US-08-79-599-3
US-08-779-599-3
Sequence 3, Application US/08779599
Patent No. 6500922
Patent No. 6500922
GENERAL INFORMATION:
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                                                                                                                                                                                                                           Score 701; DB 2; Length 2121;
Pred. No. 2e-164;
0; Mismatches 200; Indels 237;
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larity 71.0%;
Conservative
  INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 2121 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
                                                                                                                                                  Linear
                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                              Query Match
Best Local Simi
Matches 1068;
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Sequence 3, Application PC/TUS9506639
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
TITLE OF INVENTION: Tumor Necrosis Factor Receptor-Associated INFORMER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS: ADDRESSE: ADDRESSE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
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COMPUTER READABLE FORM:
COMPUTER: 3.5 inch 1.44 Mb disk
COMPUTER: 1BM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06639
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
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                                                                                                                                                                                                                                                                                                                                  Score 701; DB 4; Length 2121;
Pred. No. 2e-164;
0; Mismatches 200; Indels 237;
  TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-3216
TELEPAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2121 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
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Best Local Similarity 71.0%;
Matches 1068; Conservative
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US-08-779-599-3
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                                                                                                                                                 NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REGISTRATION NUMBER: 39,055
REPERNICH/DOCKET NUMBER: 897P2PCT
TELECOMMUNICATION INFORMATION:
TELEPAN: 415,725-3216
TELEFAX: 910,711-7168
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 212 bases
FILING DATE: 27-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/331394
FILING DATE: 28-OCT-1994
ATTORNEY/AGENT INFORMATION:
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Matches 1068; Conservative
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30B CAPRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/16980
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 5;
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Pred. No. 4.5e-64;
0; Mismatches 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/367,540
FILING DATE: 30-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 05311/0:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                            PC-DOS/MS-DOS
                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 2380 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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(617)542-8906
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TELERAX: (617)542-8906
TELEX: 100254
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                    COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
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PCT-US95-16980-2
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GENERAL INFORMATION:
APPLICANT: Brigham & Women's Hospital
TITLE OF INVENTION: CONTROLLING TRAF-MEDIATED SIGNALS
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: Boston
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                       23.4%; Score 296.6; DB 3; 66.2%; Pred. No. 4.5e-64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches 224;
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (76)..(1326)
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: U19261 Genbank
DATABASE ENTRY DATE: 1995-02-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1243 GCCATTGTGGA 1253
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Matches 444; Conservative
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PCT-US95-16980-2
                                                                                                                                                                                                                                                                                                           ; DATABASE EN
US-09-167-109-1
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766 ATGCCTGACTTGGAGCAGAAGGTCTTGGAGAATGGAGGCATCCACCTACGATGGGGTCTTC
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Jian Ni and Jing-Shan Hu
TITLE OF INVENTION: Human Genes, Sequences and
Expression Products
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CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
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MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: 18M PS/2
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CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/705,77
FILING DATE: August 30, 1996
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REGISTRATION NUMBER: 33,073
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SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
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Patent No. 6639052
GENERAL INFORMATION:
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COUNTRY: USA
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                                 | CTTTTTCAGAGGCCAGTCAACGACATGCAAGCGGCTGCCCCTCTTCTGCCCC
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TITLE OF INVENTION: Human Genes, Sequences and
TITLE OF INVENTION: Expression Products
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESSE: CARELLA, BYRNE, BAIN, GILFILLIAN, ADDRESSEE: CRECHI, STEWAR, & OLSTEIN
STREET: 6 BECKER FARM ROAD
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NAME: MULLIN, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 325800-346 (PF196)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 973-1100
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APPLICATION NUMBER: US/08/705,771
FILING DATE: August 30, 1996
CLASSIFICATION: 536
ATORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
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MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
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Patent No. 6054289
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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EDNESS: single
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: NEW JERSEY
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TACCTGAACGGCGACGGCACCGGGCGAGGAACACACCTGTCCCTCTTCTTTGTGGTGATG 1005
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                                                                                                                                                                                                                                                                                                                                                                                                                 945 AGCCTCTTCTCCCCAGCCTTCTACACTGCCAAGTATGGCTACAAGTTGTGCCTGCGGGCTG 1004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1245 crcagcaaacrdcagrcaccaagcacgccracgraaggacgacacaargrrccrcaagr 1304
                                                                                                                                                                                                                                                                                                                   886 GCCATCTTCTCCCCAGCCTTCTACACCAGCAGGTACGGCTACAAGATGTGTCTGCGTATC 945
825 criegecaagcriegagcagegerriegecercaregagegegecerecriegaregeaerrire
                                                                                                        885 CTGTGGAAGATCACCAGTGTCACCAGGCGGTGCCATGAGTCGGCCTGTGGCAGGACCGTC
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 973-994-1700
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1066 CTCGACCAGAATAACCGGGGAGCACGTGATTGACGCCTTCAGGCCCGACGTGACTTCATCC 1125
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Pred. No. 5.5e-58;
0; Mismatches 240; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: patin (Genetech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/331,394
                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
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CLASSIFICATION: 436
PRIOR APPLICATION DATE:
APPLICATION NUMBER: 08/250858
FILING DATE: 27-MAY-1994
ATTORNEY/AGENT INFORMATION:
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TELEPHONE: 415/225-3216
TELEFAX: 415/952-9881
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INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
TOWNTH: 2088 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Dreger, Ginger R. REGISTRATION NUMBER: 33 REFERENCE/DOCKET NUMBER:
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429; Conservative
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STRANDEDNESS: single
TOPOLOGY: linear
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TUMBER OF SEQUENCES:
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21.8%; Score 276.8; DB 4; Length
Best Local Similarity 64.3%; Pred. No. 3.7e-59;
Matches 431; Conservative 0; Mismatches 237; Indels
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Patent No. 5670319
GENERAL INFORMATION:
APPLICANT: Goeddel, David V.
APPLICANT: Rothe, Mike
TITLE OF INVENTION: Tumor Necrosis Factor
TITLE OF INVENTION: Receptor-Associated Factors
                                                        INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2361 base pairs
TYPE: nucleic acid
STRANDENESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
                  TELEFAX: 973-994-1744
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                       RESULT 14
US-08-446-915-1
US-08-446-915-1
Sequence 1, Application US/08446915
Fatent No. 5741667
Fatent No. 574167
Fatent No.
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COMPUTER READABLE FORM:

MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk

COMPUTER: IBM PC compatible

COMPUTER: PC-DOS/MS-DOS
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SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,915
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APPLICATION NUMBER: 00/250858
FILING DATE: 2-7 MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/331394
FILING DATE: 28-0CT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
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CTTGACCAGAACCAGAGCATGCTATTGATGCCTTCCGGCCTGACCTCAGCCTCAGCC 1312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S-06-250-858-1
Sequence 1, Application US/08250858
Sequence 1, Application US/08250858
Sequence 1, Application US/08250858
Sequence 1, Application
Sequence 1, Application
APPLICANT: Rothe, Mike
TITLE OF INVANTION: Tumor Necrosis Factor Receptor-Associated Pactors
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetiech, Inc.
STREET: 460 Point San Bruno Blvd
                                                                                                                                        TCTTTTCAGAGGCCAGTCAACGACATGAACATCGCAAGCGGCTGCCCCTTCTTCTGCCCC
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Pred. No. 5.5e-58;
0; Mismatches 240; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/250,858
FILING DATE: 27-May-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: Generated, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Dreger, Ginger R. RECISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: 85
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-3216
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 63.8
Matches 429; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: 5.25 in
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APPLICATION NUMBER:
FILING DATE:
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EDNESS: single
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APPLICANT: Rothe, Mike
TITLE OF INVENTION: TUMOR NECROSIS FACTOR RECPTOR-ASSOCIATED FACTORS
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
CITY: South San Francisco
STRATE: California
COUNTRY: USA
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Pred. No. 5.5e-58;
0; Mismatches 240; Indels
                                                                                                                                                                                                                                                                                                                                                                                                           CCMPUTER READSLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: 1BM PC compactible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/744,139
FILING DATE: 31-00c-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/250858
FILING DATE: 05/27/1994
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger,
REGISOTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: P0897C1
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INFORMATION POR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2088 base pairs
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Nucleic Acid
DEDNESS: Single
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US-08-744-139-1
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Best Local 8
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Pred. No. 5.5e-58;
0; Mismatches 240; Indels
    REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: 897P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-3216
TELEFAX: 910/371-7168
ITELER: 910/371-7168
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
LENGTH: 2088 bases
TYPE: nucleic acid
STRANDEDNESS: single
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Patent No. 5869612
GENERAL INFORMATION:
APPLICANT: Goeddel, David V
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Best Local Similarity 63.89
Matches 429; Conservative
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US-08-446-915-1
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ANGACCCTCCTGGGGACCAAGCTGGAAGTACCTGTGCTCCGCCTGCAGAAACGTC
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      RESULT 1
US-10-361-270-2
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                                                                                                                                                             151.8
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Sequence 1186, Ap
Sequence 3, Appli
Sequence 3, Appli
Sequence 30, Appli
Sequence 130, App
Sequence 1184, Ap
Sequence 1184, Ap
Sequence 1184, Ap
Sequence 129, App
Sequence 129, App
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Appli
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                                           November 6, 2004, 20:48:57; Search time 701 Seconds (without alignments) 9746.709 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                         Description
                                                                                                                                                                                      GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                US-10-561-270-2
US-09-962-832-121
US-10-954-125-136
US-10-067-125-2
US-10-084-749-63
US-10-085-17-330
US-10-085-117-330
US-10-085-117-329
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US-10-085-117-329
US-10-085-117-329
US-10-085-117-329
US-10-085-117-329
                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                  3611042 seqs, 2692057975 residues
                                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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1269
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Match
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                     Scoring table:
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                                                                                                                                            Minimum DB
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                                             Run on:
                                                                                                                                                                                                                                                                                                                                                                                  Result
No.
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Sequence 327, App Sequence 326, App Sequence 5702, App Sequence 5702, App Sequence 5702, App Sequence 5702, App Sequence 5613, App Sequence 5613, App Sequence 5613, App Sequence 129, App Sequence 131, App Sequence 31, App Sequence 2, Appli Sequence 3, Appli Sequence 3, Appli Sequence 1, Appli
Sequence 7, Appli
Sequence 28886, A
5 US-10-453-478-7

0 US-09-918-98-886

0 US-10-085-117-327

5 US-10-085-117-327

5 US-10-085-117-326

4 US-09-796-692-5702

6 US-10-154-8848-5702

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6 US-10-642-865-49

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US-10-207-655-102
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ALIGNMENTS

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JOURNEAU IN COURT.

APPLICANT: Woat Jun
APPLICANT: Wooters, Joseph L
APPLICANT: Wockers, Joseph L
APPLICANT: Wockers, Blloct
APPLICANT: Wockers, Blloct
APPLICANT: Olu, Yongchang
TITLE OF INVENTION: Composition and Method for Modulating an Inflammatory
TITLE OF INVENTION: Composition and Method for Modulating an Inflammatory
TITLE OF INVENTION: Response
TITLE OF INVENTION: Response
FILE REFERENCE: 22058-565
CURRENT FAPLICATION NUMBER: 60/355,183
FRIOR FILING DATE: 2002-02-08
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2.
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Pred. No. 7.5e-271;
0; Mismatches 39; Indels 237;
Sequence 2, Application US/10361270; Publication No. US20040038299A1; GENERAL INFORMATION:
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81.7%;
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Best Local Similarity 81.7
Matches 1230, Conservative
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QY 964 ACCGGGCGAGGAACACACCTGTCCTTTTGTGGTGATGAAGGGCCCGAATGACGCC 1023 Db 1201 ACCGGGCGAGGAACACACTGTCCTTTTTGTGGTGATGAAGGGCCCGAATGACGCC 1260 QY 1024 CTGTGCGGTGGCCTTCAACCAGAAGGTGACTTGTTGTGTGATGAAGAGCCCGAATAACCGG 1083 Db 1261 CTGCTGCGGTGGCCTTCAACCAGAAGGTGACCTTAATGCTGCTCGACCAGAATAACCGG 1320 QY 1084 GAGCACGTGATTGACGAGAGGTGACCTTAATGCTGCTCGACCAGAATAACCGG 1230 Db 1321 GAGCACGTGATTGACGAGCCCTTCAAGGTGACTTCATCATCCTCTTTTCAGAGGCCAGTC 1380 QY 1144 AACGACATGAACATCGCAAGCGGCCTGCCCCTTTCTCTCTTTTTCAGAGGCCAGTC 1380 Db 1321 AACGACATGAACATCGCAAGCGGCTGCCCCTTTCTGCCCCGTCTCTCTAGATGAGGCAATC 1380 QY 1144 AACGACATGAACATCGCAAGCGGCTGCCCCTTTCTGCCCCGTCTCCAAGATGAGGCA 1203 Db 1204 AAGAATTCCTACGTGGGGAGGGATGCCCCTTTCTTCTTCTTCTAGAGGCCATTGTGGACCTGACAGGG 1263 Db 1264 CTCTAA 1269 Db 1264 CTCTAA 1269 Db 1501 CTCTAA 1506	RESULT 2 15. Sequence 121. Application Us/09962832 17. TILE OF INVENTION: Caccar Gene Determination and Therapeutic Screening Using STILE REPRENCY. Sequence 120. 109-25. 120. 109-25. 120. 109-25. 120. 109-25. 120. 109-25. 120. 109-25. 120. 109-25. 120. 109-25. 120. 120. 120. 120. 120. 120. 120. 120
61 AAGACCCTCCTGGGGACCAAGCTGGAAGTACCTGTGCTCGCCTGCAGAAAGGTC 120 121 CTCCGCAGGCCCTTCCAGGCGCAGTGTGCCCGGTACTCCTCTTCTGCCTGGCCAGC 180 121 CTCCGCAGGCCCTTCCAGGCGCAGTGTGGCCACCGGTACTCCTCCTTCTGCCTGGCCAGC 180 181 ATCCTCAGGCCTTCCAGGCGCAGTGTGCCCCCGGTACTCTCTCT	CAGGG AAGGG CAGGG CAGG

Signatum

	US-00-514466-1186	43 Db 235 ATCTCAGGGCCCTCAGAACTGTGCTGCTGTGTGTGTGTGT
301 GAGAGCCTGCCGGCCGTCTGTCCCAGTGATGCACCTGGAAGGGGACCCTGAAAGAA 360 355 GAGAGCCTGCCGGCCGTCTGTCCCAGTGATGGATGCACCTGGAAGGGGACCCTGAAAGAA 414 361 TACG	TTTGCCGGGCCCCTGCTGCGGAGCAGACGTGAAGGCGCACCACGAG Structure Str	4 CAGCACGTGATTGACGCCTTCAGGCCCGACGTGACTTCATCCTCTTTTCAGAGGCCAGTC 11

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Oy 1264 CTCTAA 1269 Db 1555 CTCTAA 1560	RESULT 5 US-10-094-749-63 US-10-094-749-63 Sequence 63, Application US/10094749 ; Publication No. US20030219741A1 GENERAL INFORMATION: APPLICANT: SUGIYAMA, TOMOYASU APPLICANT: OTGUKI, TETSUJI APPLICANT: SATO, HIROYUKI APPLICANT: SATO, HIROYUKI APPLICANT: ISAII, SHIZUKO APPLICANT: TSANO, UNITONO, JUN-1CHI APPLICANT: TANAMOTO, JUN-1CHI APPLICANT: SERI, KEIICHI APPLICANT: SERI, ROGAIKO APPLICANT: SERI, NACHIKO APPLICANT: SERI, NACHIKO APPLICANT: TANACHIKA, ICHIRO APPLICANT: TANACHIKA, TCHIRO APPLICANT: OTGUKA, MOJOYUKI	APPLICANT: NAGAHARI, KENJI APPLICANT: MASUHO, YASUHIKO TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA FILE REFERENCE: 084335/0160 CURRENT APPLICATION NUMBER: US/10/094,749 CURRENT APPLICATION NUMBER: 2002-03-12 PRIOR PILING DATE: 2002-01-24 PRIOR PILING DATE: 2002-01-328381 PRIOR FILING DATE: 2001-09-14 NUMBER OF SEQ ID NOS: 3381 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 63 LENGTH: 2094 TYPED NA TYPED NA TYPE DNA	US-10-094-749-63 Query Match Best Local Similarity 81.5%; Pred. No. 2.66-240; Matches 1095; Conservative 0; Mismatches 174; Indels 75; Gaps 6; Qy 1 ATGGCTGCAGCTAGACCTCCCCTGGCTCCTGGAGTTGCTACAGCCGGCTTCTCC 60 LA ATGGCTGCAGCTAGACCTCCCCTGGCTCCTGGAGTTGCTACAGCCGGCTTCTCC 60 Qy 61 AAGACCTCCTGGGAGCCAAGTACCTGGAGTTGCTACAGCCGGCTTCTCC 104 Qy 61 AAGACCTCCTGGGGACCAAGTACCTGGAAGCTCGTGGCTCCGCTGCAGAAACGTC 120 Qy 121 CTCTGCAAGACCTCTGGAAGCTAGGAAGCCAAGTACCTGTGCTCCGCCTGCAGAAACGTC 164 Db 105 AAGACCTTCTAGAGGGGAACCAAGTTGGCAAGTACTTGTGCTCGCCTGCAGAAACGTC 164 Db 107 CTCTGCAAGACCCTAGAAGCTGGAAACCTGTGCTCCGCCTGCAGAAACGTC 164	165 CTCCGCAGGCCCTTCCAGGCGCACCGGTACTGCTCCTTCTGCCTGGCCAGG 181 ATCCTCAGCTCTGGCCACCGGTACTGCTCTCTCTTCTGCCTGGCCAGG 182 ATCCTCAGCTCTGGGCCTCAGAACTGTGCTGCTTCTAGGAGGGCATATATGAAGAA 225 ATCCTCAGCTCTGGGCCTCAGAACTGTGCTGCTTCAGGAGGGCATATATGAAGAA 241 GGCATTTTTAGAAAGCAGTTCGGCCTTCCCAGAAAATGCTGCCCGGAGGGGGTG 285 GGCATTTTTAGAAAGCAGTTCGGCTTCCCAGTAATGCAGGGGGGTG 301 GAGAGCCTGCCGGCCGTTGTCCAGTGATGCACCTGGAAGGGGACCCTGAAAGAA 345 GAGAGCTGCCGGCCGTCTGTCCCAGTGATGCACCTGGAAGGGGACCCTGAAAGAA 346 GAGAGCTGCCGGCCGTCTGTCCCAGTGATGCACCTGGAAAGGAA 347 GAGAGCTGCCGGCCGTCTGTCCCAGTGATGCACCTGGAAGGGGACCCTGAAAGAA 348 GAGAGCTGCCGGCCGTCTGTCCCAGTGATGCACCTGGAAGGAA
365 364 475 GGCCTGGTGAAAAGGAGGCCACCTGGAGCACAGTGCCGGAGAAAGC 534	365	CAGAGCCACGGGGGTCAGAGCTCCTGCAGAGGTGCGAGAGGCCTGGAGAAGAAGCGCC ACTTTGAGAACATTGTCTGCGTGCTCTGCAGAGGTGCGAGAGGGCCTGGAAGAAGACGCC ACTTTTGAGAACATTGTCTGCGTCCTGAACCGGGAGGTGGAGGGTGGCCTGCATGACTGCC GAGGCCTGCAGCCGCTGCTGCTCTGAACCGGGAGGTGGAGGGTGGCCTGACTGA	AGGTCAGGCCCTTCCAGGCGCAGTGCCCACCGGTACTGCTCCTTCTGCCTGGCCAGC TTCGCCAGGAAGCTCTGGCTGCCCACCGGTACTGCTCCTTCTGCCTGGCCAGC TTCGCCAGGAAGCTCTGGCTGGCCGCCATACCCGCCATCTTCTCCCCAGCC TTCTACACCAGGAAGCTGTGGCTGGCCGCATACCCGCCATCTTCTCCCCAGCC TTCTACACCAGGAAGCTGTGGCTGGCCGCATTCTTCTCCCCAGCC TTCTACACCAGGAAGCTGTGTGTGTGTGTGTTGTGT	1024 CTGCTGCGGTGGCCTTCAACCAGAGGTGACCTTAATGCTGGCGGAATAACGGG 1083 1315 CTGCTGCGGTGGCCTTCAACCAGAAGGTGACCTTAATGCTGCTCGACCAGAATAACCGG 1374 1084 GAGCACGTGATTGACGCCTTCAGGCCGTGACTTCTTTTCAGAGGCCAGTC 1143 1375 GAGCACGTGATTGACGCCTTCAGGCCCGACGTGATTTTTCAGAGGCCAGTC 1143 1144 AACGACATGAAAATTGCGAAGCGCCGACGTGACTTTTTTTT

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0; Mismatches
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REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: P0897C2
TELECOMMUNICATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 2121 base pairs
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TELEFAX: 415/952-9881
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STRANDEDNESS: Single
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Matches 1068; Conservative
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RESULT 6
US-10-283-500-3
Sequence 3, Application US/10283500
Publication No. US20030120043A1
GENERAL INFORMATION:

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APPLICANT: Goeddel, David V.
Rothe. Mike
TITLE OF INVENTION: Tumor Necrosis Factor Receptor-Associated Factors
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSES: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER: 13A FC compatible
COMPUTER: 13A FC compatible
COMPUTER: 13A FC compatible
COMPUTER: 13M FC compatible
COMPUTER: WhipPet: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: 13M FC compatible
COMPUTER: 13M FC compatible
COMPUTER: WhipPet: 3.5 inch, 1.43 Mb floppy
COMPUTER: WhipPet: 3.0-0ct-2002
SOFTWARE: WhipPet: 3.0-0ct-2002
CLASSIFICATION: AUNKNOWN
PRIOR APPLICATION: AUNKNOWN
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US-10-085-117-330
| Sequence 330, Application US/10085117
| Sequence 330, Application US/10085117
| Sequence 330, Application US/10085117
| Publication No. US2003023334A1
| GENERAL INFORMATION:
| APPLICANT: MORING, DAVIG W. | APPLICANT: MORING, Eric K. | TILE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER FILE REFERENCE: 529452000121 | CURRENT APPLICATION NUMBER: US/10/085,117 | CURRENT PILING DATE: 2002-02-27 | PRIOR APPLICATION NUMBER: US/09/798,586 | PRIOR FILING DATE: 2001-03-02 | NUMBER OF SEQ ID NOS: 361 | SEQ ID NO 330 | SERICE PRESENCE: PRESENCE:
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CURRENT APPLICATION WUMBER: US/10/172,118
CURRENT FILING DATE: 2002-06-14
PRIOR APPLICATION NUMBER: 60/380,770
PRIOR FILING DATE: 2002-05-14
NUMBER OF SEQ ID NOS: 2699
SEQ ID NO 1184
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APPLICANT: Roberts, Chris
APPLICANT: Van t' Veer, Laura
APPLICANT: Van de Vijver, Marc
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Publication No. US20030055015A1

GENERAL INFORMATION:
APPLICANT: Baker, Brenda F.
APPLICANT: Cowsert, Lex M.
APPLICANT: Monia, Brett P.
APPLICANT: Monia, Brett P.
TITLE OF INVENTION:
TITLE OF INVENTION: ANTISENSE MODULATION OF TRAF EXPRESSION
FILE REFERENCE: ISPH-0321
CURRENT APPLICATION NUMBER: US/10/067,125
CURRENT FILING DATE: 2002-04
PRIOR FILING DATE: 1998-10-06
NUMBER OF SEQ ID NOS: 228
SEQ ID NO 1
LENGTH: 2380
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LOCATION: (76)..(1326)
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: U19261 Genbank
DATABASE ENTRY DATE: 1995-02-21
          1228 TGCATTGTGGA 1238
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APPLICANT: Dai, Hongyue

APPLICANT: He, Yudong

APPLICANT: He, Yudong

APPLICANT: Linsley, Peter S.

APPLICANT: Linsley, Peter S.

APPLICANT: Roberts, Christopher J.

APPLICANT: Roberts, Christopher J.

APPLICANT: Van de Vijver, Marc J.

APPLICANT: Van de Vijver, Marc J.

APPLICANT: Van de Vijver, Marc J.

APPLICANT: Bernards, Rene

TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients

FILE REPERENCE: 3010-188-399

CURRENT APPLICATION NUMBER: 60/298, 918

PRIOR FILING DATE: 2002-06-18

PRIOR FILING DATE: 2002-06-18

PRIOR FILING DATE: 2002-06-14

PRIOR FILING DATE: 2002-06-14

PRIOR FILING DATE: 2002-06-14

PRIOR FILING DATE: 2002-06-14

PRIOR FILING DATE: 2002-06-14
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                                   1006 AAGGGCCCGAATGACGCCCTGCTGCGGTGGCCCTTCAACCAGAAGGTGACCTTAATGCTG
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; ORGANISM: Homo
US-10-342-887-1184
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AAGGGCCCGAATGACGCCCTGCTGCGGTGGCCCTTCAACCAGAAGGTGACCTTAATGCTG 1065
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Publication No. US2003023334A1

Publication No. US2003023334A1

APPLICANT: MORATION:

APPLICANT: Morris, David W.

TILE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER

FILE REFERENCE: 52945200121

CURRENT FILING DATE: 2002-02-27

PRIOR APPLICATION NUMBER: US/10/085,117

CURRENT FILING DATE: 2001-03-02

NUMBER OF SEQ ID NOS: 361

SOFTWARE PASSED for Windows Version 4.0

LENGTH: 2380
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Pred. No. 2.5e-76;
0; Mismatches 224; Indels
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 444; Conserva'
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   CTCGACCAGAATAACCGGGAGCACGTGATTGACGCCTTCAGGCCCGACGTGACTTCATCC
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Publication No. US2003208043A1
GENERAL INFORMATION:
APPLICANT: Paul Moore, Reiner Gentz, Hongjin Ji,
APPLICANT: Paul Moore, Reiner Gentz, Hongjin Ji,
TITLE OF INVENTION: Human Genes, Sequences and
TITLE OF INVENTION: Expression Products
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CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
CECCHI, STEWART & OLSTEIN
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FILING DATE: August 30, 1996
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 325800-346 (PF196)
TELECOMMUNICATION INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYBE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING WSYSTEM: MS-DOS
SOFFWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/453,478
FILING DATE: 04-Unn-2003
CLASSIFICATION: 536
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STREET: 6 BECKER FARM ROAD
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SEQUENCE CHARACTERISTICS:
LENGTH: 2361 base pairs
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STATE: NEW JERSEY
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US-10-453-478-7
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TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
TITLE REPERENCE: 92-0028 US
CURRENT APPLICATION NUMBER: US/10/044,090
CURRENT FILING DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 850
SEQ ID NOS: 850
SEQ ID NO 823
LENGTH: 5981
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883 CTGTGGAAGATCACCAATGTCACCAGGCGGTGCCATGAGTCGGCCTGTGGCAGGACCGTC 942
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llarity 66.2%; Pred. No. 3.1e-76;
Conservative 0; Mismatches 224; Indels 3;
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; CTHER INFORMATION: Incyte ID No. US20020137081A1 228001.3
US-10-044-090-823
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Publication No. US20020137081A1
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
FEATURE:
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US-10-044-090-823
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Best Local, S:
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APPLICANT: Engelhard, Eric K.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER FILE REFERENCE: 529452000121
CURRENT PILING DATE: 2002-02-27
CURRENT PILING DATE: 2001-03-02
PRICR APPLICATION NUMBER: US 09/798,586
PRICR APPLICATION NUMBER: US 09/798,586
PRICR PILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 361
SOFTWARE: FRAELSEQ for Windows Version 4.0
SEQ ID NO 327
                                                                                                                                                                                                                                                                                                     Length 481;
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Pred. No. 3.4e-69;
0; Mismatches 240; Indels
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ilarity 100.0%; Pred. No. 2.6e-69;
Conservative 0; Mismatches 0;
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NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 26886
LENGTH: 481
                                                                                                  TYPE: DNA
CRGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(481)
CTHER INFORMATION: n = A,T,C or G
US-09-918-995-28886
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al Similarity 63.8%;
429; Conservative
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; ORGANISM: Mus musculus
US-10-085-117-327
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272; Conserv
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US-10-085-117-327
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US-09-1918-995-28886/c
is Sequence 28886, Application US/09918995
i Publication No. US20030073623A1
i GENERAL INFORMATION:
i APPLICANT: Hyseq, Inc.
i TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
i TITLE OF INVENTION: REAM VARIOUS CDNA LIBRARIES
i FILE REPERINCE: 20411-756
i CURRENT PILICATION NUMBER: US/09/918,995
i CURRENT PILING DATE: 2001-07-30
i PRIOR APPLICATION NUMBER: US/09/235,076
i PRIOR FILING DATE: 1999-01-20
                                                                                                                                                                             Score 276.8; DB 15; Length
Pred. No. 1.6e-70;
0; Mismatches 237; Indels
                                                   TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO:
          TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                21.8%;
                                                                                                                                                                                Query Match
Best Local Similarity 64.3
Matches 431, Conservative
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1066 CTCGACCAGAATAACCGGGAGCACGTGATTGACGCCTTCAGGCCCGACGTGACTTCATCC 1125
1027 CTTGACCAGAACAACCGAGAGCATGCTATTGATGCCTTCCGGCCTGACCTGAGCTCAGCT 1086 946 TACCTGAACGGCACGGCACCGGGCGAGGAACACACCCTGTCCTTCTTGTGGTGATG 1005 1006 AAGGCCCGAATGACGCCCTGCTGCTGCCCTTCAACCAGAAGGTGACCTTAATGCTG 1065 967 AGAGGAGAATACGATGCTCTCCTGCCTGGCCTTCAGGAACAAGGTCACCTTTATGCTA 1026 766 ATGGCTGACTTGGAGCAGAAGGTCTTGGAGGATGGAGGCATCCACCTACGATGGGGTCTTC 825 727 CTGGGCAAGCTTGAGCACAGTCTGCGACTCATGGAGGAGGAGCATCCTTTGATGGTACTTTC 786 787 creredakadricaccakrercaccakadodereccakoakarcadrereredecedeacrere 846 1207 TGCATTGTGGAC 1218 1243 GCCATTGTGGAC 1254 OP à ΩD Op Dp Dp ઠે ð dd ò ò à ДD ò

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Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a Not1-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCWNSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LROIL225
full-length cDNA clone CSODK009YH01 of HeLa cells Cot 25-normalized of Homo sapiens (human).
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MRO-BT200
AL547385
BX398226
285299 MA
K-EST0184
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(Dases, 1 to 2193)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization
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4069342 B
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BG385770 602454002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
                                          CO573496 A
AAG19651 v
BG429315 A
CF612915 B
BM797025 B
BM305193 V
CK94910 4
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/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CSODX009YHO1"

/tissue_type="HeLa cells Cot 25-normalized"

/plasmid="pCMVSPORT_6"
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larity 84.2%; Pred. No. 1.2e-235;
Conservative 0; Mismatches 1;
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HTC; CNSLT_CDNA.
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Qy 904 TTCTACACCAGGAGATACGGCTACAGAGATGTCTCTGCGTATC Db 1164 TTCTACACCAGCAGGTACGGCTACAGATGTCTCTGCGTATC Qy 964 ACCGGGCAGGAACACCTGTCCTTCTTTGTCTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTGT	Db 1524 CTCTAA 1529 RESULT 2 BU553823 LOCUS BU553823 LOCUS BU553823 LOCUS BU553823 ACCESSION BU553823 ACCESSION BU553823 VEDETON PER SEQUENCE.	 found through the I.M.A.G.E. Consortium/LINIZ http://image.llhi.gov Plate: LLCM2766 row; m column: 04 High quality sequence stop: 579. Location/Qualifiers Location/Qualifiers / organism="Homo sapiens" / mol_type="mana" / db_xref="taxon:9606" / clone="InAGE:580972" / tissue_type="teratocarcinoma, cell / lab.hoge="PHIOB (phage-resistant)" / lone lib="NHI McC.109" / note="Torgan: ovary; Vector: pOTB7; Xhoi; const and by oligord Torinang into constructed bilabracory of Gerand M. Rubin (Univ Babracory of Gerand M. Rubin (Univ Barkeley) using ZAP-CDNA synthesis Superscript II RT (Life Technologie
61 AAGACCTCCTGGGGACCAAGCTGGAAGCCAAGTACCTGTGCTCCGCCTGCAGAACGTC 120 84 AAGACCTCCTGGGGACCAAGCTGGAAGCCAAGTACCTGTGCTCCGCCTGCAGAAACGTC 143 121 CTCCGCAGGCCCTTCCAGGCCCAGTGTGGCCAGTTCTCTCTC	GGCCTGGTCCGCCTTGGTGAAAAGGAGCGCCACCTGGAGCACGAGTGCCCGGAGAAGC CTGAGCTGCCGGCATTGCCGGGGCACCCTGCTGCGAGAGACGTGAAGGCGCACCACCACGAGG GTCTGCCCCAAATTGCCCTAAAATTGCAGAGCAGA	 ACTITIOAGAACAITGICTGCGTCCTGAACCGGGAGGTGGAGGGGGGGGCCATGACTGCC ACTITIOAGAACAITGICTGCGTCCTGAACCGGGAGGTGGAGGGGGGGGGG
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Hominidae; Homo.
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Corporation
on information can be
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/mol type="mRNA"
/db xref="table."
/db xref="table."
/db xref="table."
/lab_nost="DHIOB (TI) phage-resistant)"
/lab_nost="DHIOB (TI) phage-resistant)"
/clone_lib="NUI CGAP Shn4"
/note="Organ: Skin; Vector: pCWV-SPORT6; Site_I: NotI;
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Locatach; Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov

Tissue Procurement: James Claver, M.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.lln.gov

Plate: LLAM10600 row: f column: 12

High quality sequence stop: 847.
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GI:13908401
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Best Local Similarity 97.8%; Pred. No. 6.3e-175; Matches 831; Conservative 0; Mismatches 13; Indels 6; Gaps 5;	OY 420 CGCCATCGGCTGCTCGAGACGGTGAGAAAAAAAAGGGAGGAGGAGGTGCAGTG 479	9y 480 GCTGCGGGAGCACCTGGCCATGCTACTGAGCTGCGGAGGAAAGCCCCTCTTGGG 539	Oy 540 AGACCAGAGAGTCAGAGGTCCTGCAGAGGTGCGAGAGCCTGGAGAAGAAC 599	OY 600 GGCCACTITICAGAACAITGICTGCGTCCTGAACCGGGAGGTGGAGGTGGCCCATGAC 659	Qy 660 TGCCGAGGCCTGCAGCCGGCAGCACCAGGACAAGACTAAAGCCCTGAGTAG 719 Db 670 TGCCGAGGCCTGCAGCAGCAGCAGCTGGACCAAGACAAGATTGAAGCCCTGAGTAG 611	QY 720 CAAGGTGCAGCAGCAGCAGCATTGGCCTCAAGGACCTGGCGATTGGACTTGGA 779	QY 780 GCAGAAGGTCTTGGAGATGGAGGCATCCACCTACGATGGGGTCTTCATCTGGAAGATCTC 839	QY 840 AGACTITGGCGAGGAAGCTCCAGGAAGCTGTGGCTGGCGGCATACCCGCCATCTTCTCCCC 899	Qy 900 AGCCTTCTACACCAGCAGGTACAAGATGTGTGTGTGGGGTATCTACCTGAACGGGGA 959		Oy 1020 CGCCTGCTGCTGCCCTTCAACCAGAAGGTGACCTTAATGCTGGTCGACCAGAATAA 1079	1080 CCGGGAGCACGTGATTGACGCCTTCAGGCCGGACGTGACTTCATCCTCTTTTCAGAGGCC 1 250 CCGGGAGCACGTGATTGACGCCTTCAGGCCCGACGTGACTTCATCCTCTTTTCAGAGGCC 1	OY 1140 AGTCAACGACGAACGAACGGCTGCCCCTCTTCTGCCCCGTCTCCAAGATGGA 1199	Qy 1200 GGCAAAGAATTCCTACGTGCGGACGATGCCATCTCATCAAGGCCATTGTGACCTGAC 1259	Qy 1260 AGGCTCTAA 1269 	RESULT 5 AK052934 LOCUS AK052934 LOCUS DEFINITION Mus musculus 16 days neonate heart cDNA, RIKEN full-length enriched library, clone:D830048A10 product:Tnf receptor-associated factor 2, full insert semisore	ACCESSION AK052934 VERGION AK052934.1 GI:26343104 KEYWORDS HTC; CAP trapper
	Qy 938 IGCGIAICTACCTGAACGCCGACGGCGAGGAAGAACACACCTGTCCTTTTG 997	Oy 998 TGGTGATGAGGCCCGAATGACGCCCTGCTGCGGTGGCCCTTCAACCAGAAGGTGACCT 1057	OY 1058 TAATGCTGCTCGACCAGAATAACCGGGAGCACGTGATTGACGCCTTCAGGCCCGACGTGA 1117	Qy 1118 CTTCATCCTTTTCAGAGGCCAGTCAACGACA-TGAACATCGCAAGCGGCTGCCCCTC 1176	1177 TTCTGCCCC-GTCTCCAAGA-TGGAGGAAAGAATTCCTACGTGCGGGACGATGCCATCT 1234	1235 TCATCAAGGCCATTGTGG 1252 		DEFINITION BX328304 Home sapiens HELA CELLS COT 25-NORMALIZED Home sapiens ACCESSION BX328304 Green Service Se	S EST: G1.30310370 S EST: Homo sapiens (human) ISM Homo sapiens	EMERATYCEA MetaZoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo. REFERENCE 1 (bases 1 to 906) AUTHORS LiW B., Gruber C., Jessee J. and Polayes, D. TITLE FILL FORTH COMM STANDARD COMMENTED COMMEN	AL	BP 191 91006 EVRY cedex - France Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and Rook V sites of the prowiscoper & vector Ishery.	was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 5308.f	http://www.g	Source 1.306 /organisme"Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="tSOBXROOPHOI" /col +vre="HFLA CRIO" SE-NOBMALITED"	/cell_line="HELA" /clone_lib="Homo sapiens HELA CELLS COT 25-NORWALIZED" /note="lst strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized,"	ORIGIN Query Match 60.6%; Score 769; DB 5; Length 906;

SOURCE ORGANISM	Mus musculus Mus musculus Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,	
REFERENCE AUTHORS TITLE JOURNAL MEDLINE PUBMED	Mammalla, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. Carninci, P. and Hayashizaki, Y. High-efficiency full-length, cDNA cloning Meth. Enzymol. 303, 19-44 (1999) 10349636	
AUTHORS TITLE JOURNAL MEDLINE	E. Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes decome Res. 10 (10), 1617-1630 (2000) R 20499374 R 1042159	
REFERENCE AUTHORS	3) Shibata, K., Itoh, M., Alzawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Fujiwake, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Obara, E., Watahiki, M.,	
TITLE JOURNAL MEDLINE PITEMED	Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Vazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000) 1107.584-1	
REFERENCE AUTHORS TITLE JOURNAL	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium. Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)	
REFERENCE AUTHORS TITLE	5 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team. Analysis of the mouse transcriptome based on functional annotation 6 60, 770 full-length ConAs Nature 420, 663-573 (2002)	
REFERENCE AUTHORS	<pre>E (Dases 1 to 2993) S Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furunc, M., Hanagaki, T., Hara, A., Hashizume, W., Fukuda, K., Hayatsu, N., Hirancto, K., Hiracka, T., Hirozane, T., Hori, F., Imotani, K., Ishi, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katch, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamira, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,</pre>	
; ; ;	Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H.,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,T., Tomaru,T., Yasunishi,A.,	
JOURNAL	Subsitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Vokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-māil:genome-res@gsc.riken.jp, //genome.gsc.riken.jp/, Tel:81-45-503-9222,	
COMMENT	CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to	
FEATURES	Please visit our web site for further details. URL:http://genome.gsc.riken.jp/. URL:http://fantom.gsc.riken.jp/. I.coation/Qualifiers 12993	

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The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

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Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in Riken
Division of Experimental Animal Research in Riken contributed to
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
Location/Qualifiers
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                                                                                                                                                                                Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning Meth. Enzymol. 303, 19-44 (1999) 99279253
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AK038136 and and all by mRNA linear HTC 03-APR-2004 was musculus 16 days neonate thymus cDNA, RIKEN full-length enriched library, clone:Al30081B14 product:Tnf receptor-associated factor 2, full insert sequence.

DEFINITION

RESULT 6 AK038136

AK038136 AK038136.1 GI:26332438 HTC; CAP trapper.

ACCESSION VERSION KEYWORDS

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779 543 839

603 899 663

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AY413598 17-DEC-2003
Homo sapiens TRAF2 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
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FQACCHRYCSFCLIFSLISSSPQNCAACVYEGLYEEGISILESSAFPDMARREYES
LPAVCPNDGCTWKGTLKEYESCHEGLCPFLLTECPACKGLVRLSEKEHHTEQECPKRS
LSCOGHRAPCSHYDLEWHYEVORFPHTCDGGCKKKTRRFFYRDEYPSCRCNLCRF
HTVGCSEMVETENLQDHELQRLREHLALLLSSFLEAQASPGTLNQVGPELLQRCQILE
QXIATFENIVCYLNRSYRVAYTAAGACSRQRRLDQNKIEALSNKQQLERGIGLKOLA
MADLEQKVSELEVSTYDGVFTWKISPFTRKRQRAVAGRTPAIFSRYGYRDGLA
RVYLNGGCTGRGTHLSLFFVVWKGPNDALLQWPRQKYTMLLDHNNREHVIDAFRPD
VTSSSFQRRVSDWAINIASGCPLFCPVSKWRAKNSYYRDDAIFIKAIVDLTGL"
2092. .2097
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="unnamed protein product; Inf receptor-associated factor 2 (MGD|MGI:101835, GB|L35303, evidence: BLASIN, 99%, match=2097)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAGACCCTCCTGGGGACCAGGTTAGAAGCCAAGTACCTCTGTTCAGCCTGCAAAAACATC
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Pred. No. 5e-158;
0; Mismatches 201; Indels 237;
                                                                                                                                                                                                                                                                                                                                  enriched
/organism="Mus musculus"

mol_type="mRNA"
strain="C57BL/6J"

db_xref="FANTOM DB:Al30081B14"

db_xref="taxon:10090"

clone="Al30081B14"
                                                                                                                                                                                                                                                                                      tissue_type="thymus"
clone_lib="RIKEN full-length
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50. 1565
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Best Local Simil
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	Db 481 CTGAGCTGCCGGCATTGCCGGGCACCTGCTGCGGAGCAGACGTGAAGGCGCACCACGAG		Qy 365 - AGTITICAGGACCACGICAAGACITIGIGGCAAGIGICGGAGTCCCTIGCAGATICCACGCC	Qy 424 ATCGGCTGCCTCGAGACGCTAGAGAAACAGCAGGAGCACGAGGTGCAGTGCCTG	Qy 484 CGGGAGCACCTGGCCATGCTAGGAGCTCGGTGCTGGAGAGAAGCCCCTCTTGGGAGAC Do 721 CGGGAGCACCTGGCCATGCTAACTGAGCTCGGTGCTGGAGGCAAGCCCCTCTTGGGAGAC	9y 544 CAGAGCGAGGGGTCAGAGCTCCTGCAGAGGAGGAGGAGGAGAAGAAGAAGACGGCC	Oy 604 ACTITIGAGAACAITGICTGCGTCCTGAACCGGGAGGTGGAGAGGTGGCATGACTGCC	Qy 664 GAGGCCTGCAGCCGGCAGCAGCAGCAGCAGACAAGATTGAAGCCTGAGTAGCAAG IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	724	Db bb b	QY 784 AAGGICTIGGAGAIGGAGCAICCACCIACGAIGGGGICTICAICIGGAAGAICTCACACAC Db 1021 NNYANANANANANANANANANANANANANANANANANAN	; Oy 844	1081	OY 904 TICTACACCAGCAGGTACGGCTACAAGATGTGTGTGTGTGTTCTACCTGAACGGCGACGGC Db 1141 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN	Qy	QY 1024 CTGCTGCGGTGGCCCTTCAACCAGAAGGTGACCTTAATGCTGGTCGACCAGAATAACGGG	Db 1261	Oy 1084 GAGCACGTGATTGACGCCTTCAGGCCCGACGTGACTTCTTTTCAGAGGCCAGTC	QY 1144 AACGACATGAACATCGCAAGCGGCTGCCCCCTCTTCTGCCCCGTCTCCAAGATGGAGGCA 1381 AACGACATGGAACATCGCAAGCGGCTGCCCCCTCTTCTGCCCCGTCTCCAAGATGGAGGCA	QY 1204 AAGAATTCCTACGTGCGGGACGATGCCATCTTCATCAAGGCCATTGTGGACCTGGCAGGG	1264	Db 1501 CTCTAA 1506
ιυ O	A7413598.1 GT:39769560 GSS. Homo sapiens (human)	no sapiens daryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, mmalia. Entheria, Drimates, Cristalia, Instituto Instituto de Control de Contro	1 (bases 1 to 1506) Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Tanenbaum,D.M., Civello,D.R., Lu,P., Murphy,B., Boxxion, B.	.l.M. L.M. evolution from human-chimp-mouse o	14671302 2 (bases 1 to 1506) Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,	Lu, F., Murphy, E. C. C., Sninsky, J.	Dublicated (18-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USB. This sequence was made by sequencing genomic exons and ordering them based on alignment.	Location/Qualifiers 11506 /organism="Homo sapiens" /mol type="cenomic DNA"	/db_xref="taxon:9606" /db_xref="taxon:9606" / nrssno	/gene=".xakz" /locus_tag="HCM4944"	ore 695; DB 9; Length 1506;	Conservative 0; Mismatches 327; Indels 237; Gaps 1; GacTeCaGCTAGCAGCTAGCGTGACCCCCCTGGCTCCCTGGAGTTGCTACAGCCCGGCTTCTCC 60		AAGACCTTCTGGGGACCAAGCTGGAAGCCAAGTACCTGTGCTCCGCCTGCAGAAACGTC 120	ANGACCCITCCAGGGGCAGTGTGGCCACGGTACTGCTCCTCTGCTGCTGCTCTGCTCTCTCT	TCCGCAGGCCCTTCCAGGCGCAGTGTTTTTTTTTTTTTT	ATCCTCAGCTCTGGGCCTCAGAACTGTGCTGCCTGTGTTCACGAGGGGTATATGAAGAA 240	GGCATTTCTATTTTAGAAAGCAGTTCGGCCTTCCCAGATAATGCTGCCCGCAGGGAGGTG 300 		TACG	TACGAGAGCTGCCACGAAGGCCGCTGCCGGCTCATGCTGACCGAATGTCCCGCGTGCAAA 420	GGCCTGGTCCCCTTGGTGAAAAGGACGCCATTGAAGCACACAAGAAGAAGAAAAAAAA

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                       601 GAAGGGCCCGAATGACGCCCTGCTGCGGTGGCCCTTCAACCAGAATGTGAC
                                                                                                                                                                  CD630730 666 bp mRNA linear 56071275H1 FLP Homo sapiens CDNA, mRNA sequence. CD630730
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/organism="Homo sapiens"
/mol_type="mRNA"
/db xref="taxon:9606"
/clone_lib="FLP"
/note="Vector: pDrive Cloning Vector"
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Pred. No. 2.9e-145;
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3160 Porter Dr., Palo Alto, CA 94304,
Tel: 6508454102
Email: gfudincyte.com.
Location/Qualifiers
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1. (bases 1 to 668)
1. G., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L. Circular rapid amplification of cDNA ends for high-throughput Genomics 84 (1), 205-210 (2004)
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/db_xref="teaxon:9606"
/clone lla="FLP"
/noce="Vector: pDrive Cloning Vector"
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                                                                                                                                                                                                                                                                                                                                                                                                      Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102.
Email: gfu@incyte.com.
Location/Qualifiers
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                                                                                                      CD630731.1 GI:40278997
                                                                                                                                                       Homo sapiens (human)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. B. 1 (bases 1 to 937)

Eu (bases 1 to 937)

Mational Institutes of Health, Mammalian Gene Collection (MGC)

Lungublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: Ggapbs-r@mail.nih.gov

Tissue Procurement: Dr. David Rowe contact: Robert Strausberg, Ph.D.

Email: Ggapbs-r@mail.nih.gov

Tissue Procurement: Dr. David Rowe contact: Robert Strausberg, Ph.D.

Email: Ggapbs-r@mail.nih.gov

Tissue Procurement: Dr. David Rowe contact: Marayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Biosciance Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Linl at:

http://inage.llnl.gov

Plate: LinMi4079 row: a column: 16

High quality sequence stop: 648.
                                                                                                                                                                                                                                                                                                                                                                                                                              GIGGIGAIGAAGGGCCCGAAIGACGCCCIGCIGCGGGCCCTICAACCAGAAGGIGACC 1056
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/note="Vector: pCMV-SPORT6.1; Site 1: EcoRV; Site_2: NotI;

/cloned undifferentially. Primer: Oligo dT. Average insert

size 1.7 %b. Constructed by ResGen, Invitrogen Corp. Note:

this is a NIH_MGC Library."
                                                                                                                                                                                       241 CGCATACCCGCCATCTTCTCCCCAGCCTTCTACACCAGCAGGTACGGCTACAAGATGTGT 300
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/mol_type="mRNA"

/mol_type="mRNA"

/done="refe"="Accoration of the state of the st
                                                                     945 CTACCTGAACGGCGACGGCACCGGGCGAGGAACACACCTGTCCCTCTTTTTGTGGTGAT 1004
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186 CGCCATCTTCTCCCCAGCCTTCTACACCAGCAGGTACGGCTACAAGATGTGTCTGCGTAT 127
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,

Mamaalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

NH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: The I.M.A.G.E. Consortion
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov.b column: 17
Plate: LLCM2888 row: b column: 17
High quality sequence stop: 659.
I. Coation/Qualifiers
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AGENCOURT 10474335 NIH_MGC_107 Homo sapiens cDNA clone IIMAGE:647537 5', mRNA sequence.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E 1 (Base 1 to 578)

Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,

Kim, Y.S.

ZIC Frontier Korean EST Project 2001

Unpublished (2002)

Contact: Kim YS.

Genome Research Center

Korea Research Center

Korea Research Institute of Bioscience & Biotechnology

S. Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea

Tel: +82-42-860-4409

Email: yongsungsmail-kribb.re.kr

Plate: 8 row: D column: 01

High quality sequence stop: 578.

Location/Qualifiers

1. 578

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K-EST0070221 S22SNU16n1 Homo sapiens cDNA clone S22SNU16n1-8-D01
5., mRNA sequence.
BM790399
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                                                                                              1;
                                                  Length 937;
                                                                                              Indels
                                             Score 577.2; DB 5;
Pred. No. 1.5e-128;
0; Mismatches 168;
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		AGGTGACCTTAATGCTGCTCGACCAGAATAACCGGGAGCACGCGTTTGACGCCTTCAGGC	CCGACGTGACTTCATCCTCTTTCGGAGGCCAGTCGACGACATGAACATGGCAGCGGCT	GCCCCCTCTTCTGCCCCGTCTCCAAGATGCAGGCAAAG 1206	GCCCCCTCTTCTGCCCCCGTCTCCAAGATGGAGGCCAAAG				AY413599.1 GI:39769561	<pre>troglodytes (chimpanzee) troglodytes</pre>	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.	Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,	Feithera's., manglys, latengya.n., white, i.u., Shinsky, u.u., Adams, M.D. and Cargill, M. Inferring nonneutral evolution from human-chimp-mouse orthologous	gene trios Science 302 (5652), 1960-1963 (2003)	14671302 2 (bases 1 to 1335) Clark & G. Glandicki S. Nioleon D. Thomas D. Voississi N	Clary, Todd M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Civello, D.R., Lu, F., Murphy, B.,	Adams, M.D. and Cargill, M. Direct Submission	H ()	11335 /organism="Pan troglodytes" /mol type="genomic DNA"	/db_xref="taxon:9598" <1	ocns	39.3%: Score 498.6: DR 9: Instarth	imilarity 56.0%; Pred. No. 1.66-109; Conservative 0; Mismatches 350; Indels 237; Gaps	TGCTACAGCCCGGCTTCTCCAAGACCCTCCTGGGGACCAAGC 82	CCCTGGCTCCCTGGAGTTGCTACAGCCCGGCTTCTCCAAGACCCTCCTGGGGACCAAG	TGGAAGCCAAAGTACCTGTGCTCCAGAAACGTCCTCCGCAGGCCCTTCCAGGCGC		AGTGTGGCCACCGGTACTGCTCCTTCTGCCTGGCCAGCATCCTCAGCTCTGGGCCTCAGA	AGTGTGGCCACCGGTACTGCTCTTCTGCCTGGCCAGCATCTCAGCTCTGGGCCTCAGGCCCAGA	

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Homo sapiens

Bukaryota; Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa, Chordates; Crarrhini; Hominidae; Homo.

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Dias 1 to 495)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Brinnes, M.R.,

Magai, M.A., da Silva, W. Uz., Zago, M.A., Bordin, S., Costa, F. F.,

Goldman, G. H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,

Brunstein, A., deolivaira, P.S., Bucher, P., Jongeneel, C.V.,

Simpson, A.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
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Exa: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
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                                                                                                                                                        182 GGAGAGGAGCATCGGCCTCAAGGACCTGGCCATGGCTGACCTGGAGCAGAAGGTCTCAGA
             CCGGCAGCACCGGCTGGACCAAGACAAGATTGAAGCCCTGAGTAGCAAGGTGCAGCAGCT
                                          GATGGAGGCATCCACCTACGATGGGGTCTTCATCTGGAAGATCTCAGACTTCGCCAGGAA
                                                                                                                                                                                                                                                                                                                                        302 ACGICAGGAAGCCATCGCTGGCCGGACACCTGCTATCTTCTCCCCAGCCTTCTTCACAAG
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                                                                                                           GGAGAGGAGCATTGGCCTCAAGGACCTGGCGATGGCTGACTTGGAGCAGAAGGTCTTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                    362 CAGATATGGCTACAAGATGTCTCTCCGGGTCTACTTGAATGGCGACGGCACTGGCGGG
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010,
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                                                                                                                                                                                                                          710 bp mRNA linear EST 22-JAN-2004
AGENCOURT 17837571 NIH MGC 238 Rattus norvegicus cDNA clone
IMAGE:7131710 5', mRNA sequence.
CK596664
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/tab host="DHIOB TonA"
/clone lib="NH MGC 218"
/note="Organ: testis, Vector: pExpress-1; Site_1: EcoRV;
/note="Organ: testis, Vector: pExpress-1; Site_1: EcoRV;
site_2: Not!, RNA obtained from testis tissue of 8 wk old
animal. Tissues were Snap-frozen and kept at -80C before
RNA extraction and purification (Tri-reagent method). cDNA
was primed using oligo-dT primer:

the BCORV/Nobl sites of pExpress-1. Size-selection >1.4kb
resulted in an average insert size of 1.9 kb. This primary
library is normalized (non-normalized primary library is NIH MGC 237) and was constructed by Express Genomics
(Frederick, MD)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Bldg. 31 Rmi0A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Prourement: Howard acobs
CDNA Library Preparation: Express Genomics
CDNA Library Preparation: Express Genomics
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Library Arrayed by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
Plate: LiLMAIS032 row: p column: 12
High quality sequence stop: 585.
Location/Qualifiers
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Pred. No. 5.3e-107;
0; Mismatches 105; Indels
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/organism="Rattus norvegicus"
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/db_xref="taxon:10116"
/clone="IMAGE:7131710"
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Rattus norvegicus
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                                                                              GGCCCGACGTGACTT 1120
                                                                                                                           1321 GGCCCGACGTGACTT 1335
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llarity 84.3%;
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Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=RC6-OT0050-230 200-021-B06&ts3=2000-02-23&t4=1) Seq primer: puc 18 forward High quality sequence start: 9 High quality sequence stop: 397.
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38.3%; Score 486.2; DB 2; Length 495;
Best Local Similarity 99.2%; Pred. No. 1.4e-106;
Matches 488; Conservative 0; Mismatches 4; Indels 0
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Search completed: November 6, 2004, 22:02:17 Job time : 4410 secs

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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                  Copyright
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using sw model OM protein - protein search, ...

Run

November 10, 2004, 16:10:49; Search time 155 Seconds (without alignments) 976:669 Million cell updates/sec

US-10-018-030B-2

Perfect score:

1 MAAASVIPPGSLELLQPGFS........8YVRDDAIFIKAIVDLTGL 422 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2002273 segs, 358729299 residues Searched:

2002273

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

genesc<u>Tr</u>1986s:* genesc<u>Tr</u>1980s:* genescqr2000s:* genescqr2001s:* genescqr2003as:* genescqr2003as:* genescqr2003as:* A_Geneseq_23Sep04:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2004s:*

SUMMARIES

	Description	Aay71901 Human TRA	Aay98165 Human TRA	m	170	Adb80956 RING-SH c	Abr84599 TRAF2 pro	22 TNF-al	Abb57335 Mouse isc	Aar90578 Mouse TRA	Aay71902 Human TRA	4 Human	Human	Abu70784 Human adi	Aaw03147 Epstein-B	Aay98164 Human TRA		2 Human	Adl82947 Human PRO	Ado20499 Human PRO	Ado19524 Human PRO	Aao17756 Murine CD	Aar90577 Mouse TRA	Aaw27432 Human CRA	Abo07169 Human p53	Aaw27433 Human CRA
SUPERINTES	QI	AAY71901	AAY98165	AAY71903	ABO07170	ADB80956	ABR84599	N	ABB57335	AAR90578	AAY71902	ADA54134	AAB07002	ABU70784	AAW03147	AAY98164	ADF76476	ADL22912	ADL82947	AD020499	ADO19524	S	AAR90577	AAW27432	ABC07169	AAW27433
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	Score	Н	•	2047.5	2047.5	2047.5	ζ.	2047.5	1914.5	1909.5	1751	1631.5	1178	999.5	733.5	733.5		'n	ش	e,	733.5	m	N	α	722	722
Result	No.	Н	7	m	4	Ŋ	9	7	80	60	10	11	12	13	14	15	16	17			20					

Aaw27436 Human CRA	-	Aaw27431 Human CRA	Aay98166 Human TRA	Aao17757 Human CD4	Adb80964 RING-SH c	Adb80957 RING-SH c	Aaw27428 Human CRA	Aar98833 CD40 asso	Aaw03146 LMP1 asso	Abo07171 Human p53	Aaw27434 Human CRA	Aaw27435 Human CRA	Aar99259 Full-leng	Aab67615 Amino aci	Add25542 Binding d	Abu89708 Protein d	Aaw29258 Human TRA	Aaw27610 Human TRA
AAW27436	ABB57054	AAW27431	AAY98166	AA017757	ADB80964	ADB80957	AAW27428	AAR98833	AAW03146	ABO07171	AAW27434	AAW27435	AAR99259	AAB67615	ADD25542	ABU89708	AAW29258	AAW27610
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32.6	32.5	32.5	32.5	32.5	32.5	32.5	32.5	32.4	32.3	32.3	32.1	32.1	32.1	32.1	32.1	31.1	31.1	31.1
721.5	719	717.5	717.5	717.5	717.5	717.5	717.5	717	713.5	713.5	710.5	710.5	710	710	710	687.5	687.5	687.5
26	28	29	30	31	32	33	34	32	36	37	38		40	41	42	43	44	45

ALIGNMENTS

AAY71901 standard; protein; 422 AA **AAY71901**

AAY71901;

(first entry) 26-MAR-2001

Human TRAF2 splice variant TRAF2TR (TRAF2 truncated) protein.

Human; tumour necrosis factor; TNF; TRAF2-FL; inhibitor; treatment; try-receptor associated factor; TRAF2 truncated; TRAF2TR; antinflammatory; cardiant; myocardial infarction; splice variant; vasotropic; antipsoriatic; antirheumatic; antiarthritic; antidiabetic; vasotropic; antipsoriatic; antirheumatic; antiarthritic; antidiabetic; antiarteriosclerotic; immunosuppressive; Crohn's disease; psoriasis; rheumatoid arthritis; graft versus host disease; cardiovascular disease; non-insulin dependent diabetes; inflammatory bowel disease; stroke; neurodegenerative disease

Homo sapiens.

WO200066737-A1.

09-NOV-2000.

06-APR-2000; 2000WO-US009178.

99US-0131940P. 30-APR-1999; (AVET) AVENTIS PHARM PROD INC.

Clark KL; Guo K, Searfoss GH, Pagnoni MF, Ivashchenko YD,

WPI: 2001-007223/01. N-PSDB; AAD01947

New nucleic acid encoding variants of tumor necrosis factor receptor associated factors useful for inhibiting tumor necrosis factor alphaneguated pathways, and for treating Crohn's disease, psoriasis, and rheumatoid arthritis.

Claim 5; Fig 2b; 74pp; English.

The present sequence is a tumour necrosis factor (TNF)-receptor associated factor-truncated (TRAF2TR) protein which inhibits TNF alpharegulated pathways. This sequence is a natural splice variant of human TRAF2-FL (Full-length) protein. The TRAF2TR variant is useful for inhibiting diseases involving overproduction of TNFalpha, TNFalpha

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pathologies involving hyperactivation of nuclear factor kappa B (NFkB). The variant is also useful for inhibiting and treating inflammatory processes involving TNPalpha such as Crohn's disease, psoriasis, rheumatoid arthritis, graft versus host disease, non-insulin dependent diabetes, inflammatory bowel disease, and neurodegenerative diseases or cardiovascular disease such as cardiac ischaemia-reperfusion injury following myocardial infarction, coronary trery bypass surgery, cardiac transplantation or ischaemia-reperfusion injury in the central nervous system (CNS) following stroke, the progression and rupture of advanced conomary atherosclerotic plaques, development and progression of angioplasty, or apoptotic cell death of myocardial cells
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                                                                                                                                                                                                                                                                             100.0%; Score 2211; DB 4; Length 422; 100.0%; Pred. No. 1.9e-207; ive 0; Mismatches 0; Indels 0
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The present invention relates to antisense oligonucleotides (see AAA55495 nach55757) which are targeted to nucleic acids encoding a human tumour necrosis factor receptor-associated factor (TRAP). The antisense sequences comprise at least one modified internucleotide linkage, which is a phosphorothicate linkage. The oligonucleotides also include at least one modified sugar moiety such as a 2'-0-methoxyethy sugar moiety, sequences AAA55495 represent nucleotide sequences encoding human represent and sequences AAA98164-1988169 respresent the TRAFF-6 amino acid sequences. Included in the invention is a method for treating a human having a disease associated with the expression of TRAF comprising administering an antisense oligonucleotide. The reduction of jun kinase activation in cells comprises contacting the cells with an antisense oligonucleotide targeted to TRAF-6. A method for the reduction of E-Antisense oligonucleotides targeted to nucleic acids encoding human tumor necrosis factor receptor-associated factor (TRAF), useful for treating diseases associated with TRAF expression such as inflammatory diseases. 121 YESCHEGRCPLMLTECPACKGLVRLGEKERHLEHECPERSLSCRHCRAPCCGADVKAHHE 180 241 REHLAMILSSVLEAKPILGDQSHAGSBILQRCESLEKKTATFENIVCVLNREVERVAMTA 300 401 --FQDHVKTCGKCRVPCRFHAIGCLETVEGEKQQEHEVQWL 161 selectin expression in cells or tissues comprises contacting the cells or tissues with an antisense oligonucleotide targeted to TRAF-2 or TRAF-6. The antisense oligonucleotides have antiproliferative and anti-inflammatory activity and are useful for treating disorders associated with cell proliferation and inflammation. The antisense oligonucleotides may also be used as a diagnostic probe for studying gene function 9 1 MAAASVTPPGSLELLQPGFSKTLLGTKLEAKYLCSACRNVLRRPFQAQCGHRYCSFCLAS ILSSGPONCAACVHEGIYEEGISILESSSAFPDNAARREVESLPAVCPSDGCTWKGTLKE 61 ILSSGPONCAACVHEGIYEEGISILESSSAFPDNAARREVESLPAVCPSDGCTWKGTLKE 181 VCPKFPLTCDGCGKKKIPREKFQDHVKTCGKCRVPCRFHAIGCLETVEGEKQQEHEVQWL REHLAMILSSVLEAKPLIGDQSHAGSELLQRCESLEKKTATFENIVCVLNREVERVAMTA EACSROHRLDODKIEALSSKVOOLERSIGLKDLAMADLEOKVLEMEASTYDGVFIWKISD 282 FARKLQEAVAGRIPAIFSPAFYTSRYGYKMCLRIYLNGDGTGRGTHLSLFFVVMKGPNDA 342 LLRWPFNOKVTLMLLDQNNREHVIDAFRPDVTSSSFQRPVNDMNIASGCPLFCPVSKMEA 1 MAAASVTPPGSLELLQPGFSKTLLGTKLEAKYLCSACRNVLRRPFQAQCGHRYCSFCLAS Gaps 79; 92.6%; Score 2047.5; DB 3; Length 80.4%; Pred. No. 2.6e-191; iive 4; Mismatches 15; Indels Xu XS; Disclosure; Page 109-111; 170pp; English. BP, Monia 98US-00167109 Best Local Similarity 80.4 Matches 403; Conservative (ISIS-) ISIS PHARM INC Cowsert LM, 121 YE------WPI; 2000-303732/26. N-PSDB; AAASS491 Sequence 501 AA; 06-0CT-1998; BF, 301 61 123 Query Match 162 222 ò a ઠ g ò 셤 8 엄 8 g à g ò 염 à

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development and progression of congestive heart failure, endothelial cell injury following balloon angioplasty, or apoptotic cell death of myocardial cells
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                                                                                                                                                                                                                                                                                                                                  1 MAAASVTPPGSLELLQPGFSKTLLGTKLEAKYLCSACRNVLRRPFQAQCGHRYCSFCLAS
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                                                                                                                                                                                                                           79;
                                                                                                                                                                           Length 501;
                                                                                                                                                                     Score 2047.5; DB 4; Length
Pred. No. 2.6e-191;
4; Mismatches 15; Indels
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2001US-0328605P.
2002US-0357253P.
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Matches 403; Conser
                                                                                                                    Sequence 501 AA;
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10-OCT-2001; 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          엄
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is human tumour necrosis factor (TNF)-receptor associated factor-full length (TRAF2-FL) protein. TRAF2-FL has two variants, a splice variant of TRAF2 referred as "TRAF2 truncated"

(TRAF2TR) and a TRAF2 expression construct with enhanced dominant negative properties referred as "TRAF2 truncated-deleted" (TRAF2TD).

TRAF2-TR and TRAF2-TD are also capable of inhibiting TNF alpha signalling pathways. The TRAF2-TD are also capable of inhibiting diseases involving over production of TRAF2PD appearance of the variants are also useful for inhibiting and treating inflammatory processes involving typeractivation of nuclear factor kappa B (NFRB). The variants are also useful for inhibiting and treating inflammatory processes involving the TRAF2D and treating inflammatory processes involving the transplants host disease, psoriasis, rheumatory bowel disease, and neurodegenerative diseases or cardiovascular diseases such as cardial schematory broase such as cardial schematory horses and neurodegenerative diseases or cardiovascular diseases such as cardial schemata-reperfusion injury following myocardial infarction.
                                                                                                                                                                                                                                                                                                                                                                                                                             Human; tumour necrosis factor; TNF; TRAF2; inhibitor; treatment;
TNF-receptor associated factor; TRAF2 truncated; TRAF2TR;
TRAF2 truncated-deleted; TRAF2TP; antiinflammatory; cardiant; vasotropic; antisporiatic; antirheumatic; antiarthritic; antidiabetic; antiarteriosclerotic; immunosuppressive; Crohn's disease; psoriasis; antiarteriosclarotic; immunosuppressive; Crohn's disease; psoriasis; howmatorid arthritis; graft versus host disease; cardiovascular disease; non-insulin dependent diabetes; inflammatory bowel disease; stroke;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       coronary artery bypass surgery, cardiac transplantation or ischaemia-
reperfusion injury in the central nervous system (CNS) following stroke,
the progression and rupture of advanced coronary atherosclerotic plaques,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7.87
/note= "This region is absent in TRAF2TD (AAY71902)"
123. 201
/note= "This region is absent in TRAF2TR (AAY71901) and
TRAF2TD (AAY71902)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid encoding variants of tumor necrosis factor receptor associated factors useful for inhibiting tumor necrosis factor alpharegulated pathways, and for treating Crohn's disease, psoriasis, and rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clark KL,
                                                                                                                                                                                                                                                                                                                                                                                  Human TNF-receptor associated factor (TRAF2) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Guo K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Searfoss GH, Pagnoni MF, Ivashchenko YD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                       KNSYVRDDAIFIKAIVDLTGL 501
                                                                                                                                                                                                                      AAY71903 standard; protein; 501 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Fig 4b; 74pp; English
                                     KNSYVRDDAIFIKAIVDLTGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AVET ) AVENTIS PHARM PROD INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-APR-2000; 2000WO-US009178.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0131940P.
                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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                                  402
                                                                                  481
                                                                                                                                                                                                                                                                      AAY71903;
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                                                                                                                                                               RESULT 3

ANY 1993

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ANY 19
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from the patient; (b) contacting the sample with a probe for HM expression; (c) comparing the sample with a probe for HM expression; (c) comparing the results with a control; and (d) determining whether the comparison indicates a likelihood disease). (MI) is useful for identifying modulators of the p53 pathway. A probe for HM expression is useful for diagnosing breast, colon, kidney, lung and ovarian cancer, in a patient, where the cancer has greater than 25 % expression level. Modulators identified by (MI) are useful in a variety of diagnostic and therapeutic applications, where disease or disorder prognosis is related to defects in the p53 pathway, such as, angiogenesis, apoptotic or cell contiferation of the cell, so that the cell undergoes normal contiferation of the cell, so that the cell undergoes normal contiferation of the cell, so that the cell cycle. (M2) and (M3) are useful for modulating the p53 pathway such as angiogenic, also useful for treating defects in the p53 pathway such as angiogenic, apoptotic or cell proliferation disorders. The present sequence represents a human p53 pathway modifying protein
                                                                                                                                                                                                                                                                                                                                                                                                         modulating agent, by contacting an assay system comprising a purish modulating agent, by contacting an assay system comprising a purish polypeptide (human orthologue of genes that modify the p53 pathway in Dorsophila) or mucleic acid with a test agent under conditions, where but for the presence of the test agent, the system provides a reference activity, and detecting a test agent-biased activity of the assay system. Also included are modulating (M2) a p53 pathway of a cell (comprising contacting a cell defective in p53 function with a candidate modulator that specifically binds to a HP polypeptide comprising an HM amino acid sequence, where p53 function is restored), modulating (M3) a p53 pathway in a mammalian cell (comprising the cell with an agent that specifically binds an HM polypeptide or nucleic acid) and diagnosing (M4) a disease in a patient (comprising: (a) obtaining a biological sample
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EACSROHRLDQDKIEALSSKVQQLERSIGLKDLAMADLEQKVLEMEASTYDGVFIWKISD 281
                                                                                                                                                                                                       Identifying modulators of the p53 pathway for use in treating apoptotic or cell proliferation disorders, comprises screening for agents that modulate activity of a human ortholog of genes that modify the p53 pathway in Drosophila.
                                                                          RP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ILSSGPONCAACVHEGIYEEGISILESSSAFPDNAARREVESLPAVCPSDGCTWKGTLKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MAAASVTPPGSLELLQPGFSKTLLGTKLEAKYLCSACRNVLRRPFQAQCGHRYCSFCLAS
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                                                                             Funke
                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to identifying (M1) a candidate p53 pathway
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                                                                          Belvin M, Francis-Lang
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80.4%; Pred. No. 2.6e-191;
ive 4; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                         Example 2; Page 431-432; 678pp; English.
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403; Conservative
                                                                          Friedman L, Plowman GD,
                           EXELIXIS INC
                                                                                                                            WPI; 2003-156859/15.
                                                                                                                                                        N-PSDB; ACD13346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 501 AA;
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Best Local Si
Matches 403;
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                                                       401
                                                                                                                                          421 LLRWPPNOKVTLMLLDQNNREHVIDAFRPDVTSSSFQRPVNDMNIASGCPLFCPVSKMEA 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                   RING-SH 3; Gag protein, Gag late domain; P13K; actin; myosin; Hsp60; Hsp70; Hsp90; STAM1; STAM2A; STAM2B; VHS-UIM; GTPase; E2 enzyme; tsG101; cullin; RING-SH; clathrin; virucide; vaccine; antiviral; retrovirus; rhabocovirus; filovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MAAASVTPPGSLELLQPGFSKTLLGTKLEAKYLCSACRNVLRRPFQAQCGHRYCSFCLAS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ated protein complex comprising a RING-SH 3 polypeptide and polypeptide, useful for detecting cells infected with a virus, treating viral disorders caused by retroviruses, rhabdoviruses,
EACSROHRLDQDKI EALS SKVQQLERS I GLKDLAMADLEQKVRPFQAQCGHRYCSFCLAS
                                282 FARKLQEAVAGRIPAIFSPAFYTSRYGYKMCLRIYLNGDGTGRGTHLSLFFVVMKGPNDA
                                                                                                      LLRWPFNQKVTLMLLDQNNREHVIDAFRPDVTSSSFQRPVNDMNIASGCPLFCPVSKMEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92.6%; Score 2047.5; DB 7; Length
80.4%; Pred. No. 2.6e-191;
iive 4; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                  RING-SH complex related protein, SEQ ID No 30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Greener T, Moskowitz H, Reiss Y, Alroy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure, Fig 30, 176pp, English.
                                                                                                                                                                               KNSYVRDDAIFIKAIVDLTGL 422
                                                                                                                                                                                                      481 KNSYVRDDAIFIKAIVDLTGL 501
                                                                                                                                                                                                                                                                                                          ADB80956 standard; protein; 501 AA
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09-NOV-2001; 2001US-0345846P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-JUL-2002; 2002WO-US024589.
                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 another polypeptide,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 403; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; ADB80997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO2003033646-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or filoviruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unidentified.
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Gaps

79;

120 120

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The present invention relates to a purified complex comprising a lymphotoxin beta receptor (LTbetaR) polypeptide and Smac polypeptide. The lymphotoxin-beta receptor (LTbetaR) complex is useful for identifying modulators of LTbetaR activity or expression for treating or preventing cancer or an immune disorder such as autoimmune disorder, e.g. rheumatoid arthitis, systemic lupus erythematosus, Goodpasture's syndrome, Grave's disease, Hashimoto's thyroiditis, pemphigus vulgaris, myasthenia gravis, solredma, autoimmune haemolytic anaemia, autoimmune thrombocytopenic purpura, polymyositis, dermatomyositis, pernicious anaemia, Sjogren's syndrome, ankylosing spondylitis, vasculitis, or type I diabetes mellitus. The present sequence is a TRAFZ protein, which forms part of the complex of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 YESCHEGROPIMLTECPACKGLVRIGEKERHLEHECPERSISCRHCRAPCCGADVKAHHE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein complex; tumour necrosis factor alpha receptor; INF-alpha; INFR; nuclear factor; NF-kappaB activating kinase; NAK; RasGAP3; transducin repeat-containing protein; TRCP1; TRCP2; antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 VCPKFPLTCDGCGKKKIPREKFQDHVKTCGKCRVPCRFHAIGCLETVEGEKQQEHEVQWL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REHLAMLLSSVLEAKPLLGDQSHAGSELLQRCESLEKKTATFENIVCVLNREVERVAMTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              361 ILRKLOBAVAGRIPAIFSPAFYTSRYGYKNCLRIYLNGDGTGRGTHLSLFFVVMKGPNDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LLRWPFNQKVTLMLLDQNNREHVIDAFRPDVTSSSFQRPVNDMNIASGCPLFCPVSKMEA
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                                                                                                                                                                                                                                                                                                                                                                                                                       61 ILSSGPQNCAACVHEGIYEEGISILESSSAPPDNAARREVESLPAVCPSDGCTWKGTLKE
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                                                                                                                                                                                                                                                                               Length 501;
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                                                                                                                                                                                                                                                                               Score 2047.5; DB 7;
Pred. No. 2.6e-191;
4; Mismatches 15;
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                               Disclosure; Page 6;
   or
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Best Local Similarity
Matches 403; Conserv
                                                                                                                                                                                                                                                      Sequence 501 AA;
   vasculitis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New purified lymphotoxin-beta receptor protein complex, useful for identifying modulators of lymphotoxin-beta receptor activity or expression for treating or preventing cancer or an autoimmune disorder,
                                                                                                                                  121 YESCHEGRCPLMLTECPACKGLVRLGEKERHLEHECPERSLSCRHCRAPCCGADVKAHHE
                                                                                                                                                                                 REHLAMLL.SSVLEAKPLLGDQSHAGSELLQRCESLEKKTATFENIVCVLNREVERVAMTA
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61 ILSSGPQNCAACVHEGIYEEGISILESSSAFPDNAARREVESLPAVCPSDGCTWKGTLKE
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Best Local Similarity 74.35
Marches 372; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         281
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necrosis factor (TNF) alpha
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cytostatic; inflammation; apoptosis; gene therapy; TRAF2.
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                                                                                                                                                                Lin L, Wooters JL, Nickbarg
                                                                                                                                                                                                                                                                        Disclosure; SEQ ID NO 9; 75pp; English
                                                                                           01-AUG-2003; 2003WO-US024340.
                                                                                                                   01-AUG-2002; 2002US-0400410P
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80.4%;
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N-PSDB; ADM45823.
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403; Conserv
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                                              WO2004012673-A2
                                                                                                                                         (AMHP ) WYETH
                       Unidentified
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The present invention describes a method for examining ischaemic conditions, comprising measuring the expression levels of particular genes (1) in a test sample or determining the expression profile of a gene group in the sample comprising genes selected from (1). The method is useful for examining the ischaemia or vasospastic ischaemia) by measuring expression levels of particular genes (AB199202 to AB199912, encoding the protein sequences in ABB57020 to ABB57314) or by determining the expression profile of a gene group comprising these genes. The expression indicator when screening for ischaemic condition-improving drugs or indicator when screening for ischaemic condition-improving drugs or primers for a mouse ischaemic condition related sequence, which are used in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse, ischaemia, compressive ischaemia, occlusive ischaemia, vasospastic ischaemia, ischaemic condition, ischaemic disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nagata T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON
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                                                                                                                                                                                                                ABB57335 standard; protein; 501
481 KNSYVRDDAIFIKAIVDLTGL
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301 EACSROHKLDODXIEALSNXVQQLERSIGLKDLAMADLEQXVSELEVSTYDGVFIWKISD 360
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involved in the mediation of TNF and CD40 ligand biological activities. Recombinant TRAF2 is obtd. by expression in host cells of a CDNA clone (AAT12262) isolated using a Yeast two-hybrid assay. It is used to identify inhibitors of activities of TNF-R2, CD40 and/or LMP1 oncogene, e.g. for treratment of endotoxic (septic) shock and rheumatoid arthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human, tumour necrosis factor; TNP; TRAF2; inhibitor; treatment;

TNF-receptor associated factor; TRAF2 truncated-deleted; TRAF2TD;

antiinflammatory; cardiant; mutant; muteni; mycardial infarction;
vasctropic; antipsoriatic; antirheumatic; antiarthritic; antidabetic;
antiarteriosclerotic; immunosuppressive; Crohn's disease; psoriasis;
rheumatorid arthritis; graft versus host disease; cardiovascular disease;
non-insulin dependent diabetes; inflammatory bowel disease; stroke;
neurodegenerative disease; variant; TRAF2 truncated; TRAF2TR.
                                                                                                                                                                                                                                                                                                                                                                     121 YESCHEGLCPFLLTECPACKGLVRLSEKEHHTEQECPKRSLSCQHCRAPCSHVDLEVHYE
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                                                                                                                                                                                                                                                              1 MAAASVTPPGSLELLQPGFSKTLLGTKLEAKYLCSACRNVLRRPFQAQCGHRYCSFCLAS
                                                                                                                                                                                                                                                                                                1 MAAASVISPGSLELLQPGFSKILLGIRLEAKYLCSACKNILRRPFQAQCGHRYCSFCLIS
                                                                                                                                                                                                                                                                                                                                                61 ILSSGPONCAACVHEGIYEEGISILESSSAFPDDNAARREVESLPAVCPSDGCTWKGTLKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -------TQDHVXTCGKCRVPCRFHAIGCLETVEGEKQQEHEVQWL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human TRAF2TR variant, TRAF2 truncated-deleted (TRAF2TD) protein.
                                                                                                                                                                                                                   79;
                                                                                                                                                                            501;
                                                                                                                                                                            Length
                                                                                                                                                                                                                   Indels
                                                                                                                                                                        86.4%; Score 1909.5; DB 2; 74.1%; Pred. No. 8.8e-178; iive 22; Mismatches 29;
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                                                                                                                                                                        Query Match
Best Local Similarity 74.1
Matches 371; Conservative
                                                                                                                                 Sequence 501 AA;
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    involved in

                                                                                          181 VCPKFPLTCDGCGKKKIPRETFQDHVRACSKCRVLCRFHTVGCSEMVSTENLQDHELQRL
                                                                                                                                                                               EACSROHRLDQDKIEALSSKVQQLERSIGLKDLAMADLEQKVLEMEASTYDGVFIWKISD
                                                                                                                                                                                                                                                                   LILOWPENOKVILMLIDENNREHVIDAFRPDVISSSFORPVSDMNIASGCPLFCPVSKMEA
                                                                                                                                                      REHLAMLLSSVLEAKPLLGDQSHAGSELLQRCESLEKKTATFENIVCVLNREVERVAMTA
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                                                                                                                                                                                                                                                                                                                                                                     FTRKRQEAVAGRIPAIFSPAFYTSRYGYKMCLRVYLNGDGTGRGTHLSLFFVVMKGPNDA
                                                                                                                                                                                                                                                                                                                                                                                                                LLRWPFNQKVTLMLLDQNNREHVIDAFRPDVTSSSFQRPVNDMNIASGCPLFCPVSKMEA
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                                                                 - FODHVKTCGKCRVPCRFHAIGCLETVEGEKQQEHEVQWL
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/label= Leucine_zipper_region
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/label= TRAF_domain
275. .351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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94US-00331394.
95US-00446915.
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28-OCT-1994;
22-MAY-1995;
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                                                                                                                                                                                                                                                                  The present sequence is tumour necrosis factor (TNF)-receptor associated factor truncated-deleted (TRAP2TD) protein. This sequence includes the naturally occurring splice variation and a deletion at the N-terminal end of human TRAP2 protein. The TRAP2TD variant is useful for inhibiting diseases involving hyperactivation of nuclear factor kappa B (NFB). The variant is also useful for inhibiting and treating inflammatory processes involving TNFalpha such as Crohn's disease, psoriais, rheumatoid arthitis, graft versus host disease, non-insulin dependent diabetes, inflammatory bowel disease, and neurodegenerative diseases or cardiovascular disease such as cardiac ischaemia-reperfusion injury cardial infarction, coronary artery bypass surgery, cardiac transplantation or ischaemia-reperfusion injury in the central nervous system (CNS) following stroke, the progression and rupture of advanced congestive heart failure, endothelial cell injury following balloon and angioplasty, or apoptotic cell death of myocardial cells
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                                                                                                                                                                          New nucleic acid encoding variants of tumor necrosis factor receptor associated factors useful for inhibiting tumor necrosis factor alpharegulated pathways, and for treating Crohn's disease, psoriasis, and rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                          Clark KL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 336;
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                                                                                                          Guo K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79.2%; Score 1751; DB 4; L
100.0%; Pred. No. 1.7e-162;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SGCPLFCPVSKMEAKNSYVRDDAIFIKAIVDLTGL 336
                                                                                                          Searfoss GH, Pagnoni MF, Ivashchenko YD,
                                                                                                                                                                                                                                             Claim 6; Fig 3b; 74pp; English.
                                                                               (AVET ) AVENTIS PHARM PROD INC
                          06-APR-2000; 2000WO-US009178,
                                                      99US-0131940P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            al Similarity 100.
335; Conservative
                                                                                                                                   2001-007223/01.
                                                                                                                                                N-PSDB; AAD01948.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 336 AA;
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Best Local S:
Matches 335,
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ADA54134 standard; protein; 447 AA.

ADA54134

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         161
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                                                                                                                           Cytostatic; Anti-inflammatory; Osteopathic; Neuroprotective; Nootropic; Gene Therapy; human; secretory protein; membrane proteins; cancer; inflammatory disease; osteoporosis; neurological disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New polynucleotides encoding full-length polypeptides, e.g. secretory and/or membrane proteins, useful for developing medicines for diseases which the gene is involved, or as target molecules for gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MAAASVTPPGSLELLQPGFSKTLLGTKLEAKYLCSACRNVLRRPPQAQCGHRYCSFCLAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     171 ----LLLRSCHEGRCPLMLTECPACKGLVRLGEKERHLEHECPERSLSCRHCRAPCCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   207 VCVLNREV-ERVAMTAEACS-----RQHRLDQDKIEALSSKVQQLERSIGLKDLAMADLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OKVLEMEASTYDGVF1WK1SDFARKLQEAVAGR1PA1FSPAFYTSRYGYKMCLR1YLNGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----LGD-OSHAGSELLORCESLEKKTATFENI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DVKAHHEVCPKFPLTCDGCGKKKIPREKFQDQDKIEALSSKVQQLERSIGLKDLAMADLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to novel human secretory or membrane proceins (ADAS-4072-ADAS-5710) and their coding Sequences (ADAS-2433-ADAS-4071). The coding sequences are useful in the gene therapy of diseases caused by abnormalities of the proceins, e.g. cancer, inflammatory diseases, osteoporosis or neurological disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ishii S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Is
, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R,
oshikawa T, Otsuka M, Nagahari K, Masuho Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 14; SEQ ID NO 1702; 205pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HELI-) HELIX RES INST.
(REAS-) RES ASSOC BIOTECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-MAR-2002; 2002EP-00006586.
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24-JAN-2002; 2002US-0350435P.
                                                                 SEQ ID 1702
(first entry)
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Best Local Similarity 73.64
Matches 340; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yamamoto J, Isono Y,
Seki N, Yoshikawa T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2003-395539/38.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 447 AA;
                                                                 Human protein,
                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                       EP1293569-A2
                                                                                                                                                                                                                                                                                                                                                                                        .9-MAR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
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373 ISSSEQREVNDMNIASGCPLFCPVSKMEAKNSYVRDDAIFIKAIVDLTGL
                                                                                                 ABU70784 standard; protein; 326 AA
                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-103412/09.
N-PSDB; ACA57328.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  interactions, or for
obesity or diabetes.
                                                                                                                                                                                                                                                                                                                                                                                  (HYBR-) HYBRIGENICS.
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                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                   10-JUN-2003
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GTGRGTHLSLFFVVWKGPNDALLRWPFNQXVTLMLLDQNNREHVIDAFRPDVTSSSFQRP 380
                                                                                                                                                                                                                                         Human, TRAF(NC)-CA21 protein, Tumour-necrosis factor; TNF;
TNF receptor-associated factor; cell proliferation, cell differentiation,
apoptosis; inflammation, immune response, receptor-ligand binding assay.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                193 CESLEKKTATFENIVCVLNREVERVAMTAEACSRQHRLDQDKIEALSSKVQQLERSIGLK 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DLAMADLEQKVLEMEASTYDGVFIWKISDFARKLOEAVAGRIPAIFSPAFYTSRYGYKMC 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DLAMADLEQKVLEMEASTYDGVFIWKISDFARKRQEAVAGRIPAIFSPAFYTSRYGYKWC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               346 GTGRGTHLSLFFVVMKGPNDALLRWPFNQKVTLMLLDQNNREHVIDAFRPDVTSSSFQRP 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tumour necrosis factor (TNF) receptor has an important role in the regulation of cellular proliferation, differentiation, and apoptosis in inflammatory and immune responses. The present invention relates to a quantitative assay for measuring the ability of a substance to effect binding of a TNF receptor-associated factor (TNFAF) protein to its receptor. The present sequence is Human TRFAF(NC)-CA21 protein fragment, which was used in the present assay. This protein is the conserved C-terminal region (NC) of TRAF2, and possesses a C-terminal tag that is recognised by CA21 monoclonal antibody. Proteins which bind to the present sequence are detected by CA21 antibody which generates a signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quantitative assay for measuring the effect of a substance on tumor necrosis factor receptor associated factor protein interaction with it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CESLEKKTATFENIVCVLNREVERVAMTAEACSRQHRLDQDKIEALSSKVQQLERSIGLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LRIYLNGDGTGRGTHLSLFFVVMKGPNDALLRWPFNQKVTLMLLDQNNREHVIDAFRPDV
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                                                               406 VNDMNIASGCPLFCPVSXMEAKNSYVRDDAIFIKAIVDLTGL 447
                                                 VNDMNIASGCPLFCPVSKMEAKNSYVRDDAIFIKAIVDLTGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53.3%; Score 1178; DB 3;
99.6%; Pred. No. 1.5e-106;
iive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                        (BOEH ) BOEHRINGER INGELHEIM PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 7; Page 19-21; 27pp; English.
                                                                                                                                     AAB07002 standard; protein; 243 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Crute JJ;
                                                                                                                                                                                                                Human TRAF2 (NC) -CA21 protein.
                                                                                                                                                                                                                                                                                                                                                                       99WO-US019272,
                                                                                                                                                                                                                                                                                                                                                                                                 98US-00181958.
                                                                                                                                                                                         (first entry)
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Matches 229; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-451628/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 243 AA;
                                                                                                                                                                                                                                                                                                                    WO200026670-A1.
                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                       23-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                 29-OCT-1998;
                                                                                                                                                                                         17-0CT-2000
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                                                 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             receptor.
                                                                                                                                                                AAB07002;
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                                                                                                                RESULT 12
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The invention relates to a complex between two interacting proteins in adipocyte cells, given in the specification. The proteins are identified by selecting a bait protein from a known adipocyte marker and then performing a yeast 2-hybrid selection to isolate prey proteins are cooled by commences of an adipocyte cDNA library. The proteins are designated SID (RTM) (selected interacting domains) proteins. Also included are a polymetic combinant host cell expressing at least one of the interacting compound in adipocyte cells, as ID (RTM) polymetic comprising any of the 738 amino acid sequences given in the specification (including its fragment or variant), a SID (RTM) polymucleotide comprising any of the 738 amino acid sequences given in the specification (including its fragment or variant), a vector comprising the vector, a protein chip comprising the polymeticles and a computing at the SID (RTM) polymucleotide, a recombinant host cell comprising all or part of the data, listed in the specification. The complex, polymetic chip comprising the polymetices and a compounds are useful for preventing or treating metabolic disorders such as obesity or diabetes. Comprising the polymucleotides and compounds are useful for part of the data, listed in the specification. The complex is probes or primers. The complex is particularly useful for identifying selected interacting domains (SID (RTM)) for screening drugs that modulate the protein interaction, thus chip interaction, thus ship interaction, thus selected interaction, thus ship interaction, the second complex is such as a subject of the data is sequence represents a SID control of the sequence of the protein interaction, thus seminated the protein interaction, thus seminated the protein interaction, thus seminated the present sequence represents a SID control of the sequence of the present sequence of SID control of the sequence of the present sequence of SID control of the sequence of the present sequence of SID control of the sequence of the sequence of SID control o
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                       Human, prey, adipocyte, SID, selected interacting domain, anorectic, antidiabetic, protein-protein interaction, diabetes, yeast 2-hybrid assay; metabolic disorder, obesity.
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Human adipocyte Selected Interacting domain, SID, #415.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45.2%; Score 999.5; DB 6; 67.8%; Pred. No. 7.6e-89; iive 13; Mismatches 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 6; Page 249; 382pp; English.
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SFCLASILSSGPQN-----CAACVHEGIYEEGISILESSSAFPDNAARREVESLPAVCPS 109
                                                                                                                                                                                                                                                                                                                                 ---AEAGIGCPFAGVGCSFKGSPQSVQEHEVTSQTSHLNLLL 120
                                                                                                                                                                                                                                                                                                                                                                                          121 GFMKOWKARLGCGLESGPMALEQNLSDLQLQAAVEVAGDLEVDCYRAPCSESQEELALQH 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 QTLAQXDQALGKIEQSLRLMEEASFDGTFLWKITNVTRRCHESACGRTVSLFSPAFYTAK 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301 YGYKLCLRLYLNGDGTGKRTHLSLFIVIMRGEYDALLPWPFRNKVTFMLLDQNNREHAID 360
A novel human B-cell protein (AAW03147), termed Epstein-Barr induced apportein 6 or EB16, is induced by Epstein-Barr virus (EBV) infection. It appears to be the human homologue of murine tumour necrosis factor receptor associated factor TRAF1. A related novel B-cell protein (AAW03146), LAP1, was also identified. EB16 polypeptides, esp. the coil domain and C-terminal domain, can be used to inhibit LMP1-TRAF interaction. Such polypeptides, which may be obtd. by recombinant means (see also AAT31274), can be used to treat infection and control cell growth/tumourigenesis associated with LMP1-encoding viruses, partic. EBV
                                                                                                                                                                                                                                                                      ALCCAGCLSENPRIGEDQICPKCRGEDL-----QSISPGSRLRTQEKAHPEV---
                                                                                                                                                                                                                                                                                                   DGCTWKGTLKEYEFQDHVKTCGKCRVPCRFHAIGCLETVEGEKQQEHEVQWLREHLAMLL
                                                                                                                                                                                                                                                                                                                                                                                                                         -----SLEKKTATFENIVCVLNREVERVAMTABACSROHRLDODKIEALSSKVOQLE
                                                                                                                                                                                                                                                                                                                                                                                                                                            181 FWKEKLLAELEGKLRVFENIVAVLNKEVEASHLALATSIHOSOLDRERILSLEORVVELO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RSIGLKDLAMADLEQKVLEMEASTYDGVFIWKISDFARKLQEAVAGRIPAIFSPAFYTSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YGYKMCLRIYLNGDGTGRGTHLSLFFVVMKGPNDALLRWFFNQKVTLMLLDQNNREHVID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tumour necrosis factor receptor-associated factor, TRAF, human, antisense oligonucleotide, phosphorothioate, antiproliferative, anti-inflammatory, E-selectin, jun kinase.
                                                                                                                                                                                                             83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        367 AFRPDVTSSSFQRPVNDMNIASGCPLFCPVSKMEA-KNSYVRDDAIFIKAIVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 416;
                                                                                                                                                                                                             Indels
                                                                                                                                                                               33.2%; Score 733.5; DB 2; 37.8%; Pred. No. 1.3e-62; ive 65; Mismatches 109;
                                                                                                                                                                                                                                                                                                                                                               170 SSVLEAKPLLGDQSHAGSELLQR-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human TRAF1 protein sequence.
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les 156; Conservative
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                                                                                                                                                    Sequence 416 AA;
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                                                                                                                                                                                                                                                      DALLRWPFNOKVTLMLLDQNNREHVIDAFRPDVTSSSFORPVNDMNIASGCPLFCPVSKM 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Compounds and methods for controlling TRAF-mediated signals - by modulating interactions between Epstein Barr virus encoded proteins LMP1, LAP1, TNF, TNFR to inhibit lymphoblast growth and tumorigenesis.
                                          62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein 6, EBI6, LAP1, LMP1 associated protein 1;
                                                                                                                                                                                             SDFARKLQEAVAGRIPALFSPAFYTSRYGYKMCLRIYLNGDGTGRGTHLSLFFVVMKGPN
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               121 YEFQDHVKTCGKCRVPCRFHAIGCLETVEGEKQQEHEVQWLREHLAMLLSSVLEAK-PL-
                                            ---LLLRSCHEGRCPLM
                                                                       ---LGD-QSHAGSELLQRCESLEKKTATFENIVCVLNREV-ERVAMTAEAC
                                                                                                    LTECPACKGLVRLGEKERHLEHECPERSLSCRHCRAPCCGADVKAHHEVCPKFPLTCDGC
                                                                                                                                  225 S----RQHRLDQDKIEALSSKVQQLERSIGLKDLAMADLEQKVLEMEASTYDGVFIWKI
                                                                                                                                                       183 SDFARKRQEAVAGRIPAIFSPAFYTSRYGYKMCLRIYLNGDGTGRGTHLSLFFVVMKGPN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tumour necrosis factor receptor associated factor; TRAF; signal transduction; TNF, TNRF, lymphoblast; tumorigenesis; AIDS; Hodgkin's disease; Burkitt's lymphoma; naspharyngeal carcinoma; mononucleosis; Epstein-Barr virus; EBV; therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             infection membrane protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Epstein-Barr induced protein EBI6.
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                                          25 YDLVLHVPLTG-
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WPI; 2000-303732/26
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Antisense oligonucleotides targeted to nucleic acids encoding human tumor necrosis factor receptor-associated factor (TRAF), useful for treating diseases associated with TRAF expression such as inflammatory diseases.

Disclosure; Page 106-108; 170pp; English

-ASS757) Which are targeted to mucleic acids encoding a human tumour necrosis factor receptor-associated factor (TAAF). The antisense acquences comprise at least one modified internucleotide linkage, which is a phosphorothioate linkage. The oligonucleotides also include at least one modified sugar moiety such as a 2'-O-methoxyethyl sugar moiety. Sequences AAAS5490-AS5495 represent nucleotide sequences encoding human TRAF1-6, and sequences AAV38164-Y89169 represent the TRAF1-6 amino acid sequences. Included in the invention is a method for treating a human having a disease associated with the expression of FTAF comprising activation in cells comprises contacting the cells with an antisense oligonucleotide targeted to TRAF-6. Am method for the reduction of E-collectine expression in cells or tissues comprises contacting the cells or tissues with an antisense oligonucleotide targeted to TRAF-6. The method for the reduction of E-collectine expression in cells or tissues comprises contacting the cells or tissues with an antisense oligonucleotide targeted to TRAF-6. The matrisense oligonucleotides have antiproliferative and anti-inflammatory activity and are useful for treating disorders associated with cell proliferation and inflammation. The antisense oligonucleotides with any also be used as a diagnostic probe for studying gene function present invention relates to antisense oligonucleotides (see AAA55496

Sequence 416 AA;

55 SFCLASILSSGPQN-----CAACVHEGIYEEGISILESSSAFPDNAARREVESLPAVCPS 109 121 GFMKQWKARLGCGLESGPMALEQNLSDLQLQAAVEVAGDLEVDCYRAPCSESQEELALQH 180 -----SLEKKTATFENIVCVLNREVERVAMTAEACSROHRLDODKIEALSSKVQQLE 246 181 FWKEKLLAELEGKLRVFENIVAVLNKEVEASHLALATSIHQSQLDRERILSLEQRVVELQ 240 247 RSIGLKDLAMADLEQKVLEMEASTYDGVFIWKISDFARKLQEAVAGRIPAIFSPAFYTSR 306 241 QTLAQKDQALGKLEQSLRLMEEASFDGTFLWKITNVTRRCHESACGRTVSLFSPAFYTAK 300 307 YGYKMCLRIYLNGDGTGRGTHLSLFFVVMKGPNDALLRWPFNQKVTLMLLDQNNREHVID 366 301 YGYKLCLRLYLNGDGTGKRTHLSLFIVIMRGEYDALLPWPFRNKVTFMLLDQNNREHAID 360 110 DGCTWKGTLKEYEFQDHVKTCGKCRVPCRFHAIGCLETVEGEKQQEHEVQWLREHLAMLL 169 ------AEAGIGCPFAGVGCSFKGSPQSVQEHEVTSQTSHLNLLL 120 35 ALCCAGCLSENPRNGEDQICPXCRGEDL-----QSISPGSRLRTQEXAHPEV---Gaps AFRPDLSSASFORPOSETNVASGCPLFFPLSKLOSPKHAYVKDDTMFLKCIVE 413 AFRPDVTSSSFORPVNDMNIASGCPLFCPVSXMEA-KNSYVRDDAIFIKAIVD 418 Query Match 33.2%; Score 733.5; DB 3; Length 416; Best Local Similarity 37.8%; Pred. No. 1.3e-62; Matches 156; Conservative 65; Mismatches 109; Indels 83; 170 SSVLEAKPLIGDQSHAGSELLQR-----367 82 g à 임 g ò ò ò

Search completed: November 10, 2004, 16:24:55 Job time : 159 secs

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1 MAAASVTPPGSLELLQPGFSKTLLGTKLEAKYLCSACRNVLRRPFQAQCGHRYCSFCLAS
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86.6%; Score 1914.5; DB 1; Length
Best Local Similarity 74.3%; Pred. No. 6.4e-184;
Matches 372; Conservative 21; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Goeddel, David V.
APPLICANT: Goeddel, David V.
APPLICANT: Rothe, Mike
TITLE OF INVENTION: Tumor Necrosis Factor
TITLE OF INVENTION: Receptor-Associated Factors
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Generatech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCMPUTER READBLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patin (Generated)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/331,394
FILING DATE: PATOMER: 08/250858
FILING DATE: PANY-1994
FILING DATE: 27-MAY-1994
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: 33,055
REPERENCE/DOCKET NUMBER: 33,055
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US-08-691-814B-31
US-08-691-814B-35
US-08-691-814B-29
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US-09-068-2888-2
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; Sequence 4, Application US/08331394
; Patent No. 567019
; GENERAL INPORMATION:
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TYPE: amino acid
TOPOLOGY: linear
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Sequence 36, P
Sequence 3, Ar
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Sequence 18, 7
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'GgDZ 6/ptodata/1/iaa/5A_COMB.pep:*
'GgDZ 6/ptodata/1/iaa/6A_COMB.pep:*
'GgDZ 6/ptodata/1/iaa/6A_COMB.pep:*
'GgDZ 6/ptodata/1/iaa/6B_COMB.pep:*
'GgDZ 6/ptodata/1/iaa/PcTUS COMB.pep:*
'GgDZ 6/ptodata/1/iaa/PcTUS COMB.pep:*
                          version 5.1.6
- 2004 Compugen Ltd.
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US-08-260-858-4
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US-08-744-139-4
PCT-08-75-99-4
US-08-744-139-4
US-08-744-139-2
US-08-8-26-858-2
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Perfect score:
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                                                                                                                                             121 YESCHEGLCPFLLTECPACKGLVRLSEKEHHTEQECPKRSLSCQHCRAPCSHVDLEVHYE 180
                                                                                                                                                                                 ----FQDHVKTCGKCRVPCRFHAIGCLETVEGEKQQEHEVQWL 161
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Patent No. 5708142
GENERAL INFORMATION:
APPLICANT: Roche, Mike
TITLE OF INVENTION: Tumor Necrosis Factor Receptor-Associated Factors
NUMBER OF SEQUENCES:
ADDRESSEE: Genentech, Inc.
STREET: 46c Point San Bruno Blvd
CITY: South San Francisco
STREET: California
                                    ILSSGPQNCAACVHEGIYEEGISILESSSAFPDNAARREVESLPAVCPSDGCTWKGTLKE
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MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: 1 EMP C compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/08/250,858
FILING DATE: 27-May-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KNSYVRDDAIFIKAIVDLTGL 422
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REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: 897.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-3216
TELEFAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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61 ILSSGPQNCAACVHEGIYEEGISILESSSAFPDNAARREVESLPAVCPSDGCTWKGTLKE 120
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Patent No. 5741667

GENERAL INFORMATION:
APPLICANT: Goeddel, David V.
APPLICANT: Goeddel, David V.
APPLICANT: Rothe. Mike
TITLE OF INVENTION: Tumor Necrosis Factor Receptor-Associated Factors
NUMBER OF SEQUENCES:
ADDRESSEE: Geneticech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STREET: California
COUNTRY: USA
                                                                                                                                                                                                                     1 MAAASVTPPGSLELLQPGFSKTLLGTKLEAKYLCSACRNVLRRPFQAQCGHRYCSFCLAS
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                                                                                                                                                                      79;
                                                                                                                   86.6%; Score 1914.5; DB 1; Length 501; 74.3%; Pred. No. 6.4e-184; Live 21; Mismatches 29; Indels 79;
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COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: patin (denentech)
CURRENT APPLICATION DATA: US/08/446,915
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
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LENGTH: 501 amino acids
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     , TOPOLOGY: linear US-08-250-858-4
                                                                                                                                             Similarity
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                                                                                                                      Query Match
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DB 2;
                                                           COMPUTER RADDALE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winbatin (Genericch)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/744,139
FILING DATE: 31-Oct-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/250858
FILING DATE: 30-052/1994
ATTORNEY/AGENT INPORMATION:
APPLICATION NUMBER: 08/250858
FILING DATE: 05/27/1994
ATTORNEY/AGENT INPORMATION:
NAME: DEGGET, GINGER R.
REGISTRATION NUMBER: 33,055
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: 33,055
REGISTRATION NUMBER: 31,055
REGISTRATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGHAL SOI amino acidé
TYPER: Amino Acid
TYPER: Amino Acid
TYPER: Amino Acid
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Best Local Similarity 74.3*
Matches 372; Conservative
                                                   ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inc
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US-08-779-599-4
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Sequence 4, Application US/08744139

Patent No. 5869612

GENERAL INFORMATION:

APPLICANT: Goeddel, David V

APPLICANT: Rothe, Mike

TITLE OF INVENTION: TUMOR NECROSIS FACTOR RECPTOR-ASSOCIATED FACTORS
NUMBER OF SEQUENCES: 59

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genemeech, Inc.

STREET: 460 Point San Brancisco

CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MAAASVTSPGSLELLQPGFSKTLLGTRLEAKYLCSACKNILRRPFQAQCGHRYCSFCLTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 501;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86.6%; Score 1914.5; DB 1; Length 74.3%; Pred. No. 6.4e-184; cive 21; Mismatches 29; Indels
FILING DATE: 27-MAY-1994
PRIOR APPLICATION DATA:
PILING DATE: 28-OCT-1994
PILING DATE: 28-OCT-1994
ATTORNEY AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: 897P2
TELEPAN: 415/25-3216
TELEPAN: 415/25-3216
TELEPAN: 415/25-3216
TELEPAN: 415/25-3216
TELEPAN: 415/25-3216
TELEPAN: 5010/371-7168
INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
LENGTH: 501 muino acids
TYPE: amino acids
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Best Local Similarity 74.3'
Matches 372; Conservative
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TOPOLOGY: linear
US-08-446-915-4
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US-08-744-139-4
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121 YESCHEGLCPFLLTECPACKGLVRLSEKEHHTEQECPKRSLSCQHCRAPCSHVDLEVHYE 180 181 VCPKFPLICDGCGKKKIPRETFQDHVRACSKCRVLCRFHTVGCSEMVETENLQDHELQRL 240 222 BACSROHRIDODKIEALSSKVQQLERSIGLKDLAMADLEQKVLEMEASTYDGVFIWKISD 281 282 FARKLOBAVAGRIPAIFSPAFYTSRYGYKMCLRIYLNGDGTGRGTHLSLFFVVMKGPNDA 341 421 LLOWPFNOKVTLMLLDHNNREHVIDAFRPDVTSSSFORPVSDMNIASGCPLFCPVSKMEA 480 342 LLRWPFNQKVTLMLLDQNNREHVIDAFRPDVTSSSFQRPVNDMNIASGCPLFCPVSKMEA 401 1 MAAASVTSPGSLELLQPGFSKTLLGTRLEAKYLCSACKNILRRPFQAQCGHRYCSFCLTS 61 ILSSGPONCAACVHEGIYEEGISILESSSAFPDNAARREVESLPAVCPSDGCTWKGTLKE 61 ILSSGPQNCAACVYEGLYEEGISILESSSAFPDNAARREVESLPAVCPNDGCTWKGTLKE 123 -----FQDHVKTCGKCRVPCRFHAIGCLFTVEGEKQQEHEVQWL REHLAMILISSVLEAKPLLGDQSHAGSELLQRCESLEKKTATFENIVCVLNREVERVAMTA 1 MAAASVTPPGSLELLQPGFSKTLLGTKLEAKYLCSACRNVLRRPFQAQCGHRYCSFCLAS 79; Length 501; 29; Indels

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61 ILSSGPQNCAACVYEGLYEEGISILESSSAFPDNAARREVESLPAVCPNDGCTWKGTLKE 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 162 REHLAMLLSSVLBAKPLLGDQSHAGSELLQRCESLEKKTATFENIVCVLNREVERVAMTA 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                    Sequence 1 Application PC/TUS9506639
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Genentech, Inc.
APPLICANT: Genentech, Inc.
NUMBER OF INFORMATION: Tumor Necrosis Factor Receptor-Associated Factors
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STREET: Galifornia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MAAASVTSPGSLELLQPGFSKTLLGTRLEAKYLCSACKNILRRPFQAQCGHRYCSFCLTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: 3.5 inch, 1.44 Mb disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: partin (Genencech) CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US95/06639 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REGISTRATION NUMBER: 897P2PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-3216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/250858
FILING DATE: 27-MAY-1994
PRIOR APPLICATION NUMBER: 08/331394
APPLICATION NUMBER: 08/331394
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
                                                                              481 KNSYVRDDAIFIKAIVDLTGL 501
                                402 KNSYVRDDAIFIKAIVDLTGL
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INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 501 amino acids
TYPE: amino acids
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Best Local Similarity 74.3
Matches 372; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Sou
STATE: Ca
COUNTRY:
                                                                                                                                                                                 PCT-US95-06639-4
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Sequence 4, Application US/08779599
Patent No. 6500922
Patent No. 6500922
GENERAL IMPORMATION:
APPLICANT: Goeddel, David V.
APPLICANT: Goeddel, David V.
APPLICANT: Roche. Mike
TITLE OF INVENTION: Tumor Necrosis Factor Receptor-Associated Factors
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                             ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/779,599
FILING DATE: 07-Jan-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P0897C2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/ASSETT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-3216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
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Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 372; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
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TELEX: 910/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        252 KDLAMADLEQKVLEMEASTYDGVFIWKISDFARKLQEAVAGRIPAIFSPAFYTSRYGYKM 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  299 CLRLYLNGDGSGKKTHLSLFIVIMRGBYDALLPWPFRNKVTFWLLDQNNREHAIDAFRPD 358
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; Sequence 2, Application US/08250858
; Patent No. 5708142
GENERAL INFORMATION:
APPLICANT: Goeddel, David V.
APPLICANT: Rochte, Mike
TITLE OF INVENTION: Tumor Necrosis Factor Receptor-Associated Factors
NUMBER OF SEQUENCES: 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MASSSAPDENEFOFGCPPAPCODPSEPRVLCCT--ACLSENLRDDEDRICPKCRADNLHP
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38.5%; Pred. No. 1.8e-64;
Live 63; Mismatches 112; Indels
                                                                                                                                                                                           MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                          COMPUTER: INT P. COMPUTED: COMPUTED: COMPUTED: COMPUTED: COMPUTED: CONTRIBUTED: CON
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: 897P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/25-3216
TELEPRAX: 415/952-0001
South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   409 amino acids
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 38.5'
Matches 157; Conservative
                                                                                                                                                         COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
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                                          EACSRQHRLDQDKIEALSSKVQQLERSIGLKDLAMADLEQKVLEMEASTYDGVFIWKISD
                                                                                     301 BACSRQHRLDQDKIEALSNKVQQLERSIGLKDLAMADLEQKVSELEVSTYDGVFIWKISD
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Patent No. 6143507
GENERAL INFORMATION:
APPLICANT: Kehry, Marilyn R
APPLICANT: Crute, James J
APPLICANT: NUMBER: US/09/181,958
CURRENT APPLICANTION NUMBER: US/09/181,958
CURRENT FILING DATE: 1998-10-29
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                               FARKLORAVAGRIPALFSPAFYTSRYGYKMCLRIYLNGDGTGRGTHLSLFFVVMKGPNDA
                                                                                                                                                                                                                                                                                                                                                        LLRWPFNQKVTLMLLDQNNREHVIDAFRPDVTSSSFQRPVNDMNIASGCPLFCPVSKMEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 TSSSFQRÞVNDMNIASGCPLFCPVSKMEAKNSYVRDDAIFIKAIVDLTGL
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Patent No. 5670319
GENERAL INFORMATION
APPLICANT: Goeddel, David V.
APPLICANT: Rothe, Mike
TITLE OF INVENTION: Tumor Necrosis Factor
TITLES OF INVENTION: Receptor-Associated Factors
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3: Genentech, Inc.
460 Point San Bruno Blvd
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ORGANISM: human
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LENGTH: 243
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US-09-181-958-1
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US-08-331-394-2
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ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
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CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
APPLICATION NUMBER:
BILNG DATE:
APPLICATION NUMBER:
ATTORNEY/AGENT INPORMATION:
NAME:
DEGISTRATION NUMBER:
REGISTRATION NUMBER:
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER:
BEFERENCE/DOCKET NUMBER:
TELEPHONE:
TELEPHONE:
A115/225.3216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELERAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 409 amino acids
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      Rothe. Mike
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32.9%; Score 727; DB 1; Length 409; 38.5%; Pred. No. 1.8e-64; tive 63; Mismatches 112; Indels
                                                                                                                                     COMPUTER READBLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC comparatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/250,858
FILING DATE: 27-May-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: 897.1
TELECOMMINICATION INFORMATION:
TELEPHONE: 415/225-3216
STREET: 460 Point San Brunc CITY: 80uth San Francisco CTATE: California COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 409 amino acids
TYPE: amino acid
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Matches 157; Conservative
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US-08-446-915-2
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Best Local (
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Sequence 2, Application US/08446915 Patent No. 5741667 GENERAL INFORMATION: APPLICANT: Goeddel, David V.

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135 ------VPCRFHAIGCLETVEGEKQQEHEVQWLREHLAMLLSSVL,E 174
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TITLE OF INVENTION: Tumor Necrosis Factor Receptor-Associated Factors NUMBER OF SEQUENCES: 66 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MASSSAPDENEFOFGCPPAPCODPSEPRVLCCT--ACLSENLRDDEDRICPKCRADNLHP
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                                                                                                                                                                                                                                                  ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Parin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,915
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59 VSPGSPLTQEKVHSDVAEAEIMCPPAGVGCSFKGSPQSMQEHEATSQSSHLYLLLAVLKE 118
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                                                                                                                                                                                       APPLICANT: Goeddel, David V.
APPLICANT: Goeddel, David V.
APPLICANT: Rothe Mike
TITLE OF INVENTION: Tumor Necrosis Factor Receptor-Associated I
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSES: Generatech, Inc.
STREET: Generatech, Inc.
STREET: South San Francisco
STREET: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       372 VISSSFORPVNDMNIASGCPLFCPVSKMEA-KNSYVRDDAIFIKAIVD 418
359 LSSASFORPOSETNVASGCPLFFPLSKLQSPKHAYVKDDTMFLKCIVD 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32.9%; Score 727; DB 4; Length 409; 38.5%; Pred. No. 1.8e-64; ive 63; Mismatches 112; Indels '
                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUCHEARY APPLICATION DATA:
APPLICATION NUMBER: US/08/779,599
FILING DATE: 07-Jan-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         175 AKPLLGDQSHAGSELLQR-----
                                                                                              US-08-779-599-2; Sequence 2. Application US/08779599; Patent No. 6500922; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: POTELECOMMUNICATION INFORMATION TELEPHONE: 415/225-3216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                409 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERSISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                al Similarity 38.5
157; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 0 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                        USA
                                                                                                                                                                                                                                                                                                                                                                    CITY: Sou
STATE: Ca
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-779-599-2
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Best Local 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            252 KDLAMADLEQKVLEMEASTYDGVFIWKISDFARKLQEAVAGRIPAIFSPAFYTSRYGYKM 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLRIYLNGDGTGRGTHLSLFFVVMKGPNDALLRWPFNQKVTLMLLDQNNREHVIDAFRPD 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           299 CLRLYLNGDGSGKKTHLSLFIVIMRGEYDALLPWPFRNKVTFMLLDQNNREHAIDAFRPD 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59 VSPGSPLTQEKVHSDVAEAEIMCPFAGVGCSFKGSPQSMQEHEATSQSSHLYLLLAVLKE 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          119 WKSSPGSNLGSAPWALERNLSELQLQAAVEATGDLEVDCYRAPCCESQEELALQHLVKEK 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----LEKKTATFENIVCVLNREVERVAMTAEACSRQHRLDQDKIEALSSKVQQLERSIGL 251
                                                                                         APPLICANT: Goeddel, David V
APPLICANT: Goeddel, David V
APPLICANT: Rothe, Mike
TITLE OF INVENTION: TUMOR NECROSIS FACTOR RECPTOR-ASSOCIATED FACTORS
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genethech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85 LESSSAFPDNAARREVESLPAVCPSDG----CTWKGTLKEYEFQDHVKTCGKCR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MASSSAPDENEFORGCPPAPCODPSEPRVLCCT - - ACLSENLRDDEDRICPKCRADNIAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 32.9%; Score 727; DB 2; Length 409; Best Local Similarity 38.5%; Pred. No. 1.8e-64; Matches 157; Conservative 63; Mismatches 112; Indels
                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS, SOFTWARE: Wilpatin (Genentech) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/744,139 FILING DATE: 31-OCt-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P0897C1
                                               Sequence 2, Application US/08744139 Patent No. 5869612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/250858
FILLING DATE: 05/27/1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Dreger, Ginger R. REGISTRATION NUMBER: 33,055 REPERENCE/DOCKET NUMBER: P06 TELECOMMUNICATION INFORMATION: 415/225-3216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
TENGTH: 409 amir.
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                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Amino Acid
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299 CLRLYLNGDGSGKKTHLSLFIVIMRGEYDALLPWPFRNKVTFMLLDQNNREHAIDAFRPD 358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          206 HKCSVQTLLRSEGTNQQIKAHEASSAVQHVNLLKEWSNSLEKK-----VSLLQN- 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----- VAMTAEACS----- 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 145 ----LETV---EGEKQQ--EHEVQWLREHLAML--LSSVLEAKPLLGDQSHAGSELLQRC 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16 OPGFSKTLLGTKLEAKYLCSACRNVLRRPFQAQCGHRYCSFCLASILSSGPQNCAACVHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36 QGGYKERFVKT-VEDKYKCEKCHLVLCSPKQTECGHRSCESCMAALLSSSSPKCTAC-QE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94 SIVKDKV-----FKDNCCKREILALQIYCRNESRGCAEQLTLGHLLVHLKNDCHFEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         119 ------KE----YEPQDHVK-----TCGKCR--VP------CRFHAIGC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 32.4%; Score 717; DB 3; Length 543; Best Local Similarity 34.9%; Pred. No. 2.9e-63; Matches 184; Conservative 76; Mismatches 125; Indels 142;
                                            372 VISSSFORPVNDMNIASGCPLFCPVSKMEA-KNSYVRDDAIFIKAIVD 418
                                                                         76 GIYEEGISILESSSAFPDNAARREVESLPAVC--PSDGCTWKGTL-
                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                              APPLICANT: Reed, John C.
APPLICANT: Reed, John C.
APPLICANT: Sato, Takaaki
TITLE OF INVENTION: CD40 Associated Proteins
TYMER, OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ESLEKKTA--TFENIVCVLNREVER------
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/349,357
FILING DATE: 02-DEC-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US/08/697,610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMEDUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                              Sequence 2, Application US/08697610 Patent No. 6172187 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION: (619) 535-9001
TELERAX: (619) 535-9001
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 543 amiterials
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAVE: Campbell, Cathryn A. REGISTRATION NUMBER: 31,815 REFERENCE/DOCKET NUMBER: P-1 TELECOMMUNICATION INFORMATION: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 543 amino acids
amino acid
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 4370 La Jol
CITY: San Diego
STATE: California
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               119 WKSSPGSNLGSAPMALERNLSELQLQAAVBATGDLEVDCYRAPCCESQEELALQHLVKEK 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----LEKKTATFENIVCVLNREVERVAMTAEACSRQHRLDQDKIEALSSKVQQLERSIGL 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      179 ILAQLEEKLRVFANIVAVLNKEVEASHLALAASIHQSQLDREHLLSLEQRVVELQQTLAQ 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KDLAMADLEOKVLEMEASTYDGVFIWKISDFARKLQEAVAGRIPAIFSPAFYTSRYGYKW 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLRIYINGDGTGRGTHISLFFVVMKGPNDALLRWFFNQKVTLMLLDQNNREHVIDAFRPD 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MASSSAPDENEFQFGCPPAPCQDPSEPRVLCCT--ACLSENLRDDEDRICPKCRADNLHP 58
                                                                                Sequence 2, Application PC/TUS9506639
GENERAL INFORMATION:
APPLICANT: Generatech, Inc.
TITLE OF INVENTION: Tumor Necrosis Factor Receptor-Associated Factors NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Generatech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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359 LSSASFORPOSETNVASGCPLFFPLSKLQSPKHAYVKDDTMFLKCIVD 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32.9%; Score 727; DB 5; Length 409; 38.5%; Pred. No. 1.8e-64; Live 63; Mismatches 112; Indels
                                                                                                                                                                                                                                                                                                                                                     ZIP: 94080
COMPUTER READBLE FORM:
MEDLUM TYPE: 3.5 inch, 1.44 Mb disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06639
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APPLICATION DATA:
APPLICATION NUMBER: 08/250858
FILING DATE: 27-MAY-1994
PRIOR APPLICATION DATA: 08/331394
FILING DATE: 28-0CT-1994
ATTORNEY/AGENT INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REGISCOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 415/552-981
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity
Matches 157; Conservat
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CLASSIFICATION:
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                                                                                    PCT-US95-06639-2
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                                                                 RESULT 13
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November 10, 2004, 16:28:24 ; Search time 143 Seconds (without alignments) 1042.387 Million cell updates/sec
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2211
1 MAAASVTPPGSLELLQPGFS......NSYVRDDAIFIKAIVDLTGL 422
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(gnz 6/ptodata//pubpaa/US07 PUBCOMB.pep:*

(gnz 6/ptodata//pubpaa/US07 NEW PUB.pep:*

(gnz 6/ptodata//pubpaa/US06 PUBCOMB.pep:*

(gnz 6/ptodata//pubpaa/US07 NEW PUB.pep:*

(gnz 6/ptodata//pubpaa/US08 NEW PUB.pep:*

(gnz 6/ptodata//pubpaa/US08 NEW PUB.pep:*

(gnz 6/ptodata//pubpaa/US08 NEW PUB.pep:*

(gnz 6/ptodata//pubpaa/US08 PUBCOMB.pep:*

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(gnz 6/ptodata//pubpaa/US08 PUBCOMB.pep:*

(gnz 6/ptodata//pubpaa/US08 PUBCOMB.pep:*

(gnz 6/ptodata//pubpaa/US09 NEW PUB.pep:*

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1566620 segs, 353225886 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                          OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                 score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	Sequence 1, Appli	Sequence 4, Appli	Seguence 1702, Ap	Sequence 1, Appli	Sequence 2, Appli	Sequence 35, Appl	Seguence 2, Appli	Sequence 173, App	Seguence 36, Appl	Seguence 2, Appli	Seguence 166, App	Sequence 7, Appli	Sequence 103, App
SUMMARIES	£		US-10-361-270-1	US-10-283-500-4	US-10-094-749-1702	US-08-813-323A-1	US-10-283-500-2	US-10-004-378A-35	US-08-813-323A-2	US-10-116-275-173	US-10-004-378A-36	US-09-757-041-2	US-10-042-865-166	US-10-242-212-7	US-10-207-655-103
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	Query	rengra	501	501	447	266	409	543	568	568	568	543	568	567	567
	Query	March	95.6	86.6	73.8	33.0	32.9	32.7	32.5	32.5	32.5	32.4	32.3	32.1	32.1
		Score	2047.5	1914.5	1631.5	730	727	722	717.5	717.5	717.5	717	713.5	710	710
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Sequence 163, Apple Sequence 142, Apple Sequence 132, Apple Sequence 132, Apple Sequence 2, Appli Sequence 2, Appli Sequence 23, Appli Sequence 16, Appli Sequence 113, Appli Sequence 113, Appli Sequence 113, Appli Sequence 24, Appli Sequence 25, Appli Sequence 23, Appli Sequence 13, Appli Sequence 25, Appli Sequence 13, Appli Sequence 857, App	equence 8: equence 8:
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8 6 7 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	61 61
687.5 687.5	65. 65.
411111922222222222222222222222222222222	44 45

ALIGNMENTS

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Sequence 1, Application US/10361270;
Publication No. US20040038299A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Kuai, Jun
APPLICANT: Mochers, Isliott
APPLICANT: Nickbarg, Elliott
APPLICANT: Lin, Lin-Ling
FILE REFERENCE: 2008-565
CURRENT APPLICATION NUMBER: US/10/361,270
CURRENT FILING DATE: 2003-02-10
FRIOR FILING DATE: 2002-02-08
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PATENTIN Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 92.6%; Score 2047.5; DB 15; Length 501; Best Local Similarity 80.4%; Pred. No. 7e-173; Matches 403; Conservative 4; Mismatches 15; Indels 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 1
LENGTH: 501
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                                                                                                                                                                                                                                                                                                                                                                                                                                  121 YESCHEGLCPFLLTECPACKGLVRLSEKEHHTEQECPKRSLSCQHCRAPCSHVDLEVHYE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 VCPKFPLTCDGCGKKKIPRETFQDHVRACSKCRVLCRFHTVGCSEMVETENLQDHELQRL 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EACSROHRLDODKIEALSNKVOOLERSIGLKDLAMADLEOKVSELEVSTYDGVFIWKISD 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FARKLQBAVAGRIPAIFSPAFYTSRYGYKMCLRIYLNGDGTGRGTHLSLFFVVMKGPNDA 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FTRKROEAVAGRIPAIFSPAFYTSRYGYKMCLRVYLNGDGTGRGTHLSLFFVVMKGPNDA 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REHLAMLLSSVLEAKPLLGDQSHAGSELLQRCESLEKKTATFENIVCVLNREVERVAMTA 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LLRWPFNQKVTLMLLDQNNREHVIDAFRPDVTSSSFQRPVNDMNIASGCPLFCPVSKMEA 401
                                                                    1 MAAASVTPPGSLELLQPGFSKTLLGTKLEAKYLCSACRNVLRRPFQAQCGHRYCSFCLAS
                                                                                                              ------PQDHVKTCGKCRVPCRFHAIGCLETVEGEKQQEHEVQWL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EACSROHRLDQDKIEALSSKVQQLERSIGLKDLAMADLEQKVLEMEASTYDGVFIWKISD
Gaps
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Rothe, Mike
TITLE OF INVENTION: Tumor Necrosis Factor Receptor-Associated Factors
NUMBER OF SEQUENCES: 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66 ECGHRFCESCMAALLSSSSPKCTAC-QESIIXDKV-----FKDNCCKREILALQVYC 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          131 GKCR--VP------CRFHAI 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 177 SHCKSQVPMIKLQKHEDTDCPCVVVSCPHKCSVQTLLRSELSAHLSECVNAPSTCSFKRY 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                143 GCLETVEGEKQQ--EHEVQWLREHLAML--LSSVLEAKPLLGDQSHAGSELLQRCESLEK 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            237 GCV--FQGTNQQIKAHEASSAVQHVNLLKEWSNSLEKK------VSLLQN-ESVEK 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      199 KTA--TFENIVCVLNREVER------RQHR 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      230 LDQD----KIEALSSKVQQLF------------RSIGLKDLAMADLEQ 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : | : : | | : : | | : : | 344 EEADSMKSSVESLQNRVTELESVDKSAGQAARNTGLLESQLSRHDQTLSVHDIRLADMDL 403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      322 TGRGTHLSLFFVVMKGPNDALLRWPFNQKVTLMLLDQ-NNREHVIDAFRPDVTSSSFQRP 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48 QCGHRYCSFCLASILSSGPQNCAACVHEGIYEEGISILESSSAFPDNAARREVESLPAVC 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MAAASVTPPGSLELLQP-----GFSKTLLGTKLEAKYLCSACRNVLRRPFQA
                                                                                                                                                                                                                                                                                                                                                                                                                                          33.0%; Score 730; DB 8; Length 566;
llarity 32.1%; Pred. No. 8.4e-56;
Conservative 80; Mismatches 131; Indels 184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          524 TGEMNIASGCPVFVAQTVLE-NGTYIKDDTIFIKVIVDTSDL 564
ATTORNEY/AGENT INFORMATION:
NAME: White, John
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 50655
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEPHONE: (212) 379-0525
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
TENGTH: 566 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/10283500
Publication No. US2030120043A1
GENERAL INFORMATION:
APPLICANT: Goeddel, David V.
                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: Peptide
;
LOCATION: 1..566
US-08-813-323A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 187; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QKVLEMEASTYDGVFIWKISDFARKLQEAVAGRIPAIFSPAFYTSRYGYKMCLRIYLNGD 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YEFODHVKTCG------KCRVPCRFHAI------GCLETVEGEKQOEHEVQWL 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              162 REHLAMLLSSVLEAK-PL------LGD-QSHAGSELLQRCESLEKTATFENI 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          286 OKVLEMEASTYDGVFIWKISDFARKRQEAVAGRIPAIFSPAFYTSRYGYKMCLRIYLNGD 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTGRGTHLSLFFVVMKGPNDALLRWPFNQKVTLMLLDQNNREHVIDAFRPDVTSSSFQRP 380
                                                                                                                                                                                                                                                                                                                            9
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                                                                                                                                                                                                                                                                                                                                                                                                        61 ILSSGPQNCAACVHEGIYEGISILESSSAFPDNAARREVESLPAVCPSDGCTWKGTLKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MAAASVTPPGSLELLQPGFSKTLLGTKLEAKYLCSACRNVLRRPFQAQCGHRYCSFCLAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 YEVK--MPACGMVTEAPAVGSRPRSPSSYDLVLHVPLTGAEACLMSVEBETE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        207 VCVLNREV-ERVAMTAEACS-----RQHRLDQDKIEALSSKVQQLERSIGLKDLAMADLE
                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Baltimore, David
APPLICANT: Cheng, Genhong
APPLICANT: Cleary, Alieen
APPLICANT: Lederman, Seth
APPLICANT: Lederman, Seth
APPLICANT: Verores and Seth
APPLICANT: Lederman, Seth
APPLICANT: Verores and Seth
APPLICANT: Lederman, Seth
APPLICANT: Cooper & Dunham, LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                 55;
                                                                                                                                                                                          DB 14; Length 447;
                                                                                                                                                                                                                                 50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VNDMNIASGCPLFCPVSKMEAKNSYVRDDAIFIKAIVDLTGL 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VNDMNIASGCPLFCPVSKMEAKNSYVRDDAIFIKAIVDLTGL 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/813,323A
FILING DATE:
CLASSIFICATION: 530
                                                                                                                                                                                     Query Match
73.8%; Score 1631.5; DB 14
Best Local Similarity 73.6%; Pred. No. 5.3e-136;
Matches 340; Conservative 17; Mismatches 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08813323A ; Publication No. US20020031522A1
NUMBER OF SEQ ID NOS: 3381
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1702
                                                                                        ; TYPE: PRT; ORGANISM: Homo sapiens
US-10-094-749-1702
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CURRENT FILING DATE: 2100-10-24
PRIOR PULING DATE: 2001-10-24
PRIOR FILING DATE: 2001-10-24
PRIOR PLING DATE: 2000-10-24
PRIOR PELING DATE: 2000-10-24
PRIOR PELING DATE: 2000-10-24
PRIOR PELING DATE: 2000-10-24
PRIOR PELING DATE: 2001-06-22
PRIOR PAPLICATION NUMBER: 60/242,765
PRIOR PAPLICATION NUMBER: 60/242,769
PRIOR PELING DATE: 2001-06-24
PRIOR PELING DATE: 2000-10-24
PRIOR PELING DATE: 2000-10-24
PRIOR PELING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: 60/242,767
PRIOR APPLICATION NUMBER: 60/242,767
PRIOR PELING DATE: 2000-10-26
                                                                                                                                                                                                                                                                           Age, Michele
Rastelli, Luca
Shenoy, Suresh G
Grosse, William M
Alsobrook II, John P
                                                                                                         Guo, Xiaojia Sasha
Casman, Stacie J
Burgess, Catherine E
                                                                                                                                                                                                                                                                                                                                                                                              Lepley, Denise M
Gerlach, Valerie
Edinger, Schlomit
MacDougall, John R
Peyman, John A
Gunther, Erik
Stone, David J
                                                                    Patturajan, Meera
Shimkets, Richard A
                                                                                                                                                                                                                                                          Kimberly A
                                                                                                                                                                                     Malyankar, Uriel M
Tchernev, Velizar
                                                                                                                                                                                                                            Vernet, Corrine A
                        Furtak, Kazarzyna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 34.9
Matches 184; Conservative
                                                 Perna, Amanda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                            Spytek,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85 LESSSAFPDNAARREVESLPAVCPSDG----CTWKGTLKEYEFQDHVKTCGKCR---- 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           119 WKSSPGSNLGSAPMALERNLSELQLQAAVBATGDLBVDCYRAPCCESQEELALQHLVKEK 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  179 LLAQLEEKLRVFANIVAVLNKEVEASHLALASIHQSQLDREHLLSLEGRVVELQQTLAQ 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  239 KDQVLGKLEHSLRLMEBASFDGTFLWKITNVTKRCHESVCGRTVSLFSPAFYTAKYGYKL 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----LEKKTATFENIVCVLNREVERVAMTAEACSRQHRLDQDKIEALSSKVQQLERSIGL 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  252 KDLAMADLEQKVLEMEASTYDGVFIWKISDFARKLQEAVAGRIPAIFSPAFYTSRYGYKM 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLRIYLNGDGTGRGTHLSLFFVVMKGPNDALLRWPFNQKVTLMLLDQNNREHVIDAFRPD 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -VPCRFHAIGCLETVEGEKOOEHEVOWLREHLAMLLSSVLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     372 VTSSSFORPVNDMNIASGCPLFCPVSKMEA-KNSYVRDDAIFIKAIVD 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32.9%; Score 727; DB 14; Length 409; 38.5%; Pred. No. 1e-55;
                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech) CURRENT APPLICATION DATA: NS/10/283,500 FILING DATE: 30-OCt-2002 CLASSIFTCATION: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63; Mismatches
                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/779,599
FILING DATE: 07-Jan-1997
ATTORNEY/AGENT INFORMATION:
                   ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: P0897C2
TELECOMMUNICATION:
TELEPHONE: 415/225-3216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 35, Application US/10004378A Publication No. US20030228301A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 409 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 415/952-9881
TELEX: 910/371-7168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               175 AKPLLGDQSHAGSELLQR
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 157; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 6
US-10-004-378A-35
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APPLICANT: Ellerman, Karen
APPLICANT: Gangolli, Esha A
TITLE OF INVENTION: No. US20030228301A1el Human Proteins, Polynucleotides Encoding The
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 21402-179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94 SIVKDKV------FKDNCCKREILALQIYCRNESRGCAEQLILGHLLVHLKNDCHFEE 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ------KE----YEFQDHVK-----TCGKCR--VP------CRFHAIGC- 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16 OPGFSKTLLGTKLEAKYLCSACRNVLRRPFQAQCGHRYCSFCLASILSSGPQNCAACVHE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 191
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32.7%; Score 722; DB 14; Length 543; 34.9%; Pred. No. 4.1e-55; Live 77; Mismatches 124; Indels 142;
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Sequence 173, Application US/10116275

Sequence 173, Application US/2003021476A1

GENERAL INFORMATION:
APPLICANT:
Branch David
APPLICANT:
Branch Dariel J.
APPLICANT:
Branch Dariel J.
APPLICANT:
APPLICANT:
Higgins, Lisa
APPLICANT:
Higgins, Lisa
TITLE OF INVENTION:
Compositions Targeting Peyer's Patches and M Cells and Methods and TITLE OF INVENTION:
TITLE OF INVENTION:
CURRENT APPLICATION NUMBER: US/10/116,275
CURRENT FILING DATE: 2002-10-04
NUMBER OF SEQ ID NOS: 349

SOFTWARE: Patentin Version 3.1
                                                                                                                                                                                                                          264 KEWSNSLEKK------VSLLQN-ESVEKNKSIQSLHNQICSFEIEIERQKEMLRNN 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        290 VAGRIPAIFSPAFYTSRYGYKMCLRIYLNGDGTGRGTHLSLFFVVWKGPNDALLRWPFNQ 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        433 VMGKTLSLYSOPFYTGYFGYKMCARVYLNGDGMGKGTHLSLFFVIMRGEYDALLPWPFKQ 492
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -------CRFHAIGCLETVEGEKQQ--EHEVQWLREHLAML 168
                                                                                                                                                                                                                                                                                                                                                                                               206 HKCSVQTLLRSELSAHLSECVNAPSTCSFKRYĞCV--FQGTNQQIKAHEASSAVQHVNLL 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        313 ESKILHLORVIDSOAEKLKELDKEIRPFRONWEBADSMKSSVESLONRVTELESVDKSAG 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---KDLAMADLEQKVLEMEASTYDGVFIWKISDFARKLQEA
                                                                                                                 16 OPGFSKTLLGTKLEAKYLCSACRNVLRRPFQAQCGHRYCSFCLASILSSGPQNCAACVHE
                                                                                                                                                     36 OGGYKEKFVKT-VEDKYKČEKCHLVLCSPKOTECGHRFCESCMAALLSSSSPKCTAC-OE
                                                                                                                                                                                                                                                                                                                   146 LPCVRPDCXEKVLRXDLRDHVEKACKYREATCSHCKSQVPMIALQKHEDTDCPCVVVSCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     217 ------KIBALSSKVQQLE-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                       169 --LSSVLEAKPLLGDQSHAGSELLQRCESLEKKTA--TFENIVCVLNREVER-
                                     Length 568;
                                                                                                                                                                                               76 GIYEEGISILESSSAFPDNAARREVESLPAVC--PSDGCTWKGTL
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Pred. No. 1.1e-54;
                                                                                                                                                                                                                                                                               -----KE----YEFQDHVK-----TCGKCR--VP-
                                     32.5%; Score 717.5; DB 8; 33.2%; Pred. No. 1.1e-54; ive 75; Mismatches 124;
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                                                          Best Local Similarity 33.23
Matches 184; Conservative
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CRGANISM: Homo sapiens
US-10-116-275-173
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Best Local Similarity
  US-08-813-323A-2
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LENGTH: 568
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                                          Query Match
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                                                                                                                                                                                                                                                                                                    ADLEQKVLEMEASTYDGVFIWKISDFARKLQEAVAGRIPAIFSPAFYTSRYGYKMCLRIY 316
                                                                                                                                                                                                                                                                                                                                        434
                                                                                                                                                                                                                                                                                                                                                                                INGDGTGRGTHLSLFFVVMKGPNDALLRWPFNQKVTLMLLDQ-NNREHVIDAFRPDVTSS 375
146 IPCVRPDCKEKVLRKDLRDHVEKACKYREATCSHCKSQVPMIALQKHEDTDCPCVVVSCP 205
                                                             145 ----LETV---EGEKQQ--EHEVQWLREHLAML--LSSVLEAKPLLGDQSHAGSELLQRC 193
                                                                                                  ------VSLLQN- 254
                                                                                                                                                                                                                                                                                                                                                                                                       435 INGDGMGKGTHISLFFVIMRGEYDALLPWPFKQKVTIMIMDQGSSRRHLGDAFKPDPNSS 494
                                                                                                                                                                                                                      ----KDLAM
                                                                                                                                                                                                                                                                                                                           -------VAMTAEACS------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Cheng, Genhong
APPLICANT: Cleary, Alieen
APPLICANT: Lederman, Seth
APPLICANT: Ye, Zheng-sheng
TITLE OF INVENTION: TRUNCATED CRAFI INHIBITS CD40 SIGNALING
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ||::|| :||||||| : | SFKKPTGEMNIASGCPVFVAQTVLE-NGTYIKDDTIFIKVIVDTSDL 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SFORPVNDMNIASGCPLFCPVSKMBAKNSYVRDDAIFIKAIVDLTGL 422
                                                                                                                                                                                                                      -ROHRLDOD----KIEALSSKVQQLE------RSIGL-----
                                                                                                206 HKCSVQTLLRSEGTNQQIKAHEASSAVQHVNLLKEWSNSLEKK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATUR SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
APPLICATION DATA:
FILING DATE:
FILING DATE:
                                                                                                                                      ESLEKKTA--TFENIVCVLNREVER----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Cooper & Dunham, LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/08813333A Publication No. US20020031522A1 GENERAL INFORMATION: APPLICANT: Baltimore, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: White, John P
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 50659
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERIFICS:
TYPPET 568 aming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 single
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1..568
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NAME/KEY:
LOCATION:
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350 KVTLMLLDQ-NNREHVIDAFRPDVTSSFQRPVNDMNIASGCPLFCPVSKMEAKNSYVRD 408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32.5%; Score 717.5; DB 14; 33.2%; Pred. No. 1.1e-54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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Best Local Simil
Matches 184;
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                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Pat
SEQ ID NO 36
LENGTH: 568
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                                                                                                                                                                                                                                                                                                                                                                               94 SIVKDKV------FKDNCCKREILALQIYCRNESRGCAEQLTLGHLLVHLKNDCHFEE 145
                                                                                                                                                                146 LPCVRPDCKEKVLRKDLRDHVEKACKYRBATCSHCKSQVPMIALQKHEDTDCPCVVVSCP 205
                                                                                                                                                                                                                                                                             312
                                                                                                                                                                                                                                                                                                                       290 VAGRIPAIFSPAFYTSRYGYKMCLRIYLNGDGTGRGTHLSLFFVVMKGPNDALLRWPFNQ 349
                                                                                                                                                                                                                                                                                                                                                                                                                                  KVTLMLLDQ-NNREHVIDAFRPDVTSSSFQRPVNDMNIASGCPLFCPVSKMEAKNSYVRD 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QPGFSKTLLGTKLEAKYLCSACRNVLRRPFQAQCGHRYCSFCLASILSSGPQNCAACVHE 75
                                                                                                                                                                                                                                                                  -----CRFHAIGCLETVEGEKQQ--EHEVQWLREHLAML
                                                                                                                                                                                                                        206 HKCSVQTLLRSELSAHLSECVNAPSTCSFKRYGCV--FOGTNQOIKAHEASSAVQHVNLL
                                                                                 76 GIYEEGISILESSSAPPDNAARREVESLPAVC--PSDGCTWKGTL-------
                                                                                                                                                                                                                                                                                                                                                              ---RSIGL-----KDLAMADLEQKVLEMEASTYDGVFIWKISDFARKLQEA
Gaps
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75; Mismatches 124; Indels 171;
                                                                                                                                                                                                                                                                                                      ------VAMTAEACS-----RQHRLDQD----KIEALSSKVQQLE
                                                                                                                                      -----TCGKCR--VP-
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Patturajan, Meera
Shimkets, Richard A
Guo, Xiaojia Sasha
Casman, Stacie J
Burgess, Catherine E
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Tchernev, Velizar T
Vernet, Corrine A
Spytek, Kimberly A
Agee, Michele
Rastelli, Luca
Shenoy, Suresh G
Grosse, William M
Alsobrook II, John P
Lepley, Denise M
Gerlach, Valerie
Edinger, Schlomit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DTIFIKVIVDTSDL 565
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Ellerman, Karen
184; Conservative
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Gunther, Erik
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                                                                                                                                                                                                                                                                             264 KEWSNSLEKK
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APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICANT:
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APPLICANT: Gangolli, Esha A
TITLE OF INVENTION: No. US20030228301A1el Human Proteins, Polynucleotides Encoding The
TITLE OF INVENTION: No. US20030228301A1el Human Proteins, Polynucleotides Encoding The
TITLE OF INVENTION: No. US200302028301A1el Human Proteins, Polynucleotides Encoding The
TITLE OF INVENTION: NORTHER: US/10/004,378A
CURRENT APPLICATION WUMBER: 60/242,882
PRIOR FILING DATE: 2000-10-24
PRIOR PRIOR APPLICATION WUMBER: 60/242,765
PRIOR PRIOR APPLICATION WUMBER: 60/242,765
PRIOR FILING DATE: 2000-10-24
PRIOR FILING DATE: 2000-10-24
PRIOR PRIOR FILING DATE: 2000-10-24
PRIOR PRIOR APPLICATION WUMBER: 60/242,768
PRIOR PRILING DATE: 2000-10-24
PRIOR PRILING DATE: 2000-10-24
PRIOR PRILING DATE: 2000-10-24
PRIOR PRILING DATE: 2000-10-26
PRIOR APPLICATION WUMBER: 60/243,622
PRIOR APPLICATION WUMBER: 60/243,591
PRIOR PRILING DATE: 2000-10-26
PRIOR FILING DATE: 2000-10-26
PRIOR PRILING DATE: 2000-10-26
PRIOR FILING DATE: 2000-10-27
PRIOR APPLICATION WUMBER: 60/243,591
PRIOR FILING DATE: 2000-10-27
PRIOR FILING DATE: 2000-10-27 146 LPCVRPDCKEKVLRKDLRDHVEKACKYREATCSHCKSQVPMIALQKHEDTDCPCVVVSCP 205 206 HKCSVQTLLRSELSAHLSECVNAPSTČSFKRYĞČV--FQĞTNQQIKAHEASSAVQHVNLL 263 264 KEWSNSLEKK-----VSLLON-ESVEKNKSIQSLHNQICSFEIEIERQKEMLRNN 312 16 QPGFSKTLLGTKLEAKYLCSACRNVLRRPPQAQCGHRYCSFCLASILSSGPQNCAACVHE 36 QGGYKEKFVKT-VEDKYKCEKCHLVLCSPKQTECGHRFCESCMAALLSSSSPKCTAC-QE 137 ------EHEVQWLREHLAML 247 ---RSIGL-------KDLAMADLEQKVLEMEASTYDGVFIWKISDFARKLQEA 290 VAGRIPAIFSPAFYTSRYGYKMCLRIYLNGDGTGRGTHLSLFFVVMKGPNDALLRWPFNQ 169 --LSSVLEAKPLLGDQSHAGSELLQRCESLEKKTA--TFENIVCVLNREVER----217 -----VAMTAEACS-----RQHRLDQD----KIEALSSKVQQLE---75; Mismatches 124; Indels 171; Length 568; 76 GIYEEGISILESSSAFPDNAARREVESLPAVC--PSDGCTWKGTL----

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435 INGDGMGKGTHLSLFFVIMRGEYDALLPWPFXQKVTLMLMDQGSSRRHLGDAFKPDPNSS 494
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PPLICANT: Gunther, Brik
PPLICANT: Stone, David
ITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
ITLE OF INVENTION: Using the Same
                                                                                                                                                  LNGDGTGRGTHLSLFFVVMKGPNDALLRWPFNQKVTLMLLDQ-NNREHVIDAFRPDVTSS
                                                                                                                     ADLEQXVLEMEASTYDGVFIWKISDFARKLQEAVAGRIPAIFSPAFYTSRYGYKWCLRIY
                                                                                                                                                                                                                                                                                                                         376 SFORPVNDMNIASGCPLFCPVSKMEAKNSYVRDDAIFIKAIVDLTGL 422
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CURRENT APPLICATION NUMBER: US/10/042,865

CURRENT FILING DATE: 2002-05-17

PRIOR APPLICATION NUMBER: 60/260,417

PRIOR FILING DATE: 2001-01-09

PRIOR APPLICATION NUMBER: 60/272,338

PRIOR FILING DATE: 2001-01-10

PRIOR PLING DATE: 2001-01-10

PRIOR PLING DATE: 2001-02-28

PRIOR APPLICATION NUMBER: 60/274,876

PRIOR APPLICATION NUMBER: 60/274,876

PRIOR APPLICATION NUMBER: 60/274,876

PRIOR APPLICATION NUMBER: 60/284,704

PRIOR PLING DATE: 2001-03-09

PRIOR PLING DATE: 2001-04-18
                       226 -RQHRLDQD----KIEALSSKVQQLE--
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o. US20040029216A1
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Gangolli, Esha A
Burgess, Catherine E
Patturajan, Meera
Vernet, Corine A.M
Taylor, Sarah
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Miller, Charles E
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Zerhusen, Bryan D
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rosse, William M
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Shenoy, Suresh G
Spytek, Kimberly
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493 KVTLMLMDQGSSRRHLGDAFKPDPNSSSFKKPTGEMNIASGCPVFVAQTVLE-NGTYIKD 551
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/757,041
                                                                                                                                                                                                                                                                                                                                                                                                                         E: Campbell and Flores
4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                  Sequence 2, Application US/09757041
Patent No. US2002009726A1
GENERAL INFORMATION:
APPLICANT: Reed, John C.
APPLICANT: Sato, Takaaki
TITLE OF INVENTION: CD40 Associated Proteins
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ESLEKKTA - - TFENIVCVLNREVER - - - - - -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/349,357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Campbell, Cathryn A. REGISTRATION NUMBER: 31,815 REFERENCE/DOCKET NUMBER: P-1 TELECOMMUNICATION INFORMATION: (619) 535-9001
                                               409 DAIFIKAIVDLTGL 422
                                                                                               552 pririkvivorsoi 565
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amino acid
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MOLECULE TYPE: protein
US-09-757-041-2
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MEDIUM TYPE: Floppy
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STREET: 4370 La Jol
CITY: San Diego
STATE: California
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Best Local Si
Matches 181
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                                                                                                                                        146 LPCVRPDCKEKVLRKDLRDHVEKACKYREATCSHCKSQVPMIALQKHEDTDCPCVVVSCP 205
                                                                                                                                                                                                                                         --CRFHAIGCLETVEGEKQQ--EHEVQWLREHLAML 168
                                                                                                                                                                                                                                                                                                                                                                                |: || || || || || || || QVARNTGILESQLSRHDQMLSVHDIRLADMDLRFQVLETASYNGVLIWKIRDYKRRKQEA 432
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                                                                                                                                                                                                                                                                                                                                264 KEWSNSLEKK------VSLLON-ESVEKNKSIQSLHNOICSFEIEIERQKEMLRNN 312
                                                                                                                                                                                                                                                                                                                                                                                                                       -----KDLAMADLEQKVLEMEASTYDGVFIWKISDFARKLQEA 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VAGRIPAIFSPAFYTSRYGYKWCLRIYLNGDGTGRGTHLSLFFVVMKGPNDALLRWPFNQ 349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16 OPGFSKTLLGTKLEAKYLCSACRNVLRRPFQAQCGHRYCSFCLASILSSGPQNCAACVHE
                                                                            36 QGGYKEKFVKT-VEDKYKCEKCHLVLCSPKQTECGHRFCESCMAALLSSSSPKCTAC-QE
                                                                                                                                                                                                                                                                     206 HKCSVQTLLRSELSAHLSECVNAPSTCSFKRYGCV--FQGTNQQIKAHEASSAVQHVNLL
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                                 Gaps
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Publication No. US2003009644A1
GENERAL INFORMATION:
APPLICANT: AHUJA, SEEMA
APPLICANT: AHUJA, SEEMA
TITLE OF INVENTION: CD40 LIGAND AND CD40 AGONIST COMPOSITIONS AND
TITLE OF INVENTION: METHODS OF USE
FILE REFERENCE: 4003.001000
CURRENT APPLICATION NUMBER: US/10/242,212
CURRENT FILING DATE: 2002-09-12
PRIOR PEDITCATION NUMBER: US/09/645,926
PRIOR PEDITCATION NUMBER: US/09/645,926
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Version 3.0
SEQ ID NO 7
1tch 32.3%; Score 713.5; DB 15; Length 568; cal Similarity 32.7%; Pred. No. 2.5e-54; 181; Conservative 75; Mismatches 127; Indels 171;
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32.1%; Score 710; DB 14; Length 567;
Best Local Similarity 32.7%; Pred. No. 5.1e-54;
Matches 181; Conservative 74; Mismatches 128; Indels 170;
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                                                                                                                     GIYEEGISILESSSAFPDNAARREVESLPAVC--PSDGCT------
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TYPE: PRT
ORGANISM: Homo sapiens
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 Query Match
Best Local
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146 PCVRPDCKEKVLRKDLRDHVEXACKYREATCSHCKSQVPMIALQKHEDTDCPCVVVSCPH 205
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   QPGFSKTLLGTKLEAKYLCSACRNVLRRPFQAQCGHRYCSFCLASILSSGPQNCAACVHE
                                                          36 OGGYKEKFVKT-VEDKYKCEKCHLVLCSPKOTECGHRFCESCMAALLSSSSPKCTAC-OE
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APPLICANT: Ledbetter, Jeffrey A.
AITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
FILE REFERENCE: 390069,401C1
CURRENT APPLICATION NUMBER: US/10/207,655
NUMBER FILING DATE: 2002-07-25
NUMBER OF SEQ ID NOS: 4426
SOFTWARE: Patentin version 3.0
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                                                                                                                                                                                                                                                114 -----WKGTLKEYEFQDHVK------TCGKCR--VP----
                                                                                                                        GIYEEGISILESSSAFPDNAARREVESLPAVC--PSDGCT--
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181; Conservative
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US-10-207-655-103
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135 VP------ 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       247 DLHKSLEQKESKIQQLAETIKKLEKEFKQFAQLFGKNGSFLPNIQVFASHIDKSAWLEAQ 306
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PRIOR APPLICATION NUMBER: 60/260,831
PRIOR FILING DATE: 2001-01-10
PRIOR FILING DATE: 2001-02-28
PRIOR PLIANG DATE: 2001-02-28
PRIOR PLIANG DATE: 2001-02-8
PRIOR FILING DATE: 2001-02-8
PRIOR FILING DATE: 2001-04-18
PRIOR FILING DATE: 2001-04-18
NUMBER OF SEQ ID NOS: 264
SOFTWARE: PATCHIN VET. 2.1
SEQ ID NO 163
LENGTH: 538
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APPLICANT: Furtak, Kazarzyna
APPLICANT: Perna, Amanda
APPLICANT: Patturajan, Meera
APPLICANT: Shimkets, Richard A
APPLICANT: Guo, Xiaojia Sasha
APPLICANT: Gasman, Stadie J
APPLICANT: Malyankar, Uriel M
APPLICANT: Tchernev, Velizar T
APPLICANT: Vernet, Corrine A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 30.23
Matches 160; Conservative
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CRGANISM: Homo sapiens
US-10-042-865-163
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US-10-004-378A-34
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                                                                                                                                                                                                                                                                      264 EWSNSLEKK------VSLLQN-ESVEKNKSIQSLHNQICSFEIEIERQKEMLRNNE 312
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TITLE OF INVENTION: Using the Same
TITLE OF INVENTION: Using the Same
FILE REFERENCE: 21402-537
CURRENT APPLICATION NUMBER: US/10/042,865
CURRENT APPLICATION NUMBER: 002-05-17
PRIOR APPLICATION NUMBER: 60/260,417
PRIOR FILING DATE: 2001-01-09
                                                                                                        -----CRFHAIGCLETVEGEKQQ--EHEVQWLREHLAML-
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                                                                                                                                                                                                                                    169 -LSSVLEAKPLLGDQSHAGSELLQRCESLEKKTA--TFENIVCVLNREVER----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 163, Application US/10042865; Publication No. US20040029216A1; GENERAL INFORMATION:
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Gangolli, Esha A
Burgess, Catherine E
Patturajan, Meera
Vernet, Corine A.M
Taylor, Sarah
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Miller, Charles B
Boldog, Kaojia
Boldog, Rerence L
Grosse, William M
Alsobrook II, John P
Gerlach, Valerie L
Edinger, Shlomit R
Rothenberg, Mark E
Bllerman, Karen
MacDougall, John
Malyankar, Uriel M
Mallet, Isabelle
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APPLICANT: Li, Li
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Zerhusen, Bryan D
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Gunther, Erik
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Shenoy, Suresh G
Spytek, Kimberly
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134

145;

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326 VHQLLQMVNQQQNKFDLRPLMEAVDTVKQKITLLENNDQRLAVLEEETNKHDTHINIHKA 385
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                                                                                                                                                                                                                                                                                                           446 AYLNGDGSGRGSHLSLYFVVVRRGEFDSLLQWPPRQRVTLMLLDQSGKKNIMETFKPDPNS 505
   -IGLKDL 254
                                                                                                                                       255 AMADLEQKVLEMEASTYDGVFIWKISDFARKLQEAVAGRIPAIFSPAFYTSRYGYKMCLR 314
                                                                                                                                                                                                                                                                     315 IYLNGDGTGRGTHLSLFFVVMKGPNDALLRWPFNQKVTLMLLDQNNREHVIDAFRPDVTS 374
                                                                                                                                                                                                                                                                                                                                                                                                  375 SSFORPVNDMNIASGCPLFCPVSKME-AKNSYVRDDAIFIKAIVDLTGL 422
                                                                                                                                                                                                                                                                                                                                                                                                                                            506 SSFKRPDGEMNIASGCPRFVAHSVLENAKNAYIKDDTLFLKVAVDLTDL 554
      219 ---MTAEACSROHRLD----QDKIEALSSKVQQLERS-
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TITLE OF INVENTION: No. US20030228301A4el Human Proteins, Polynucleotides Encoding TH
TITLE OF INVENTION: No. US20030228301A4el Human Proteins, Polynucleotides Encoding TH
TITLE OF INVENTION: Methods of Using the Same
CURRENT PLILIAG DATE: 2001-10-24
PRIOR APPLICATION NUMBER: 60/242,882
PRIOR APPLICATION NUMBER: 60/242,882
PRIOR PILING DATE: 2000-10-24
PRIOR PELING DATE: 2000-10-26
PRIOR PELING DATE: 2000-10-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85 LESSSAFPDNAARREVESLPAVCP-SDGCTWKGTLKEYEFQDHVKTC------GKCR 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Spytek, Kimberly A
Agee, Michele
Rastelli, Luca
Shenoy, Suresh G
Grosse, William M
Alsobrook II, John P
                                                                                                                                                                                                                              Gerlach, Valerie
Edinger, Schlomit
MacDougall, John R
Peyman, John A
Gunther, Erik
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Gangolli, Esha A
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Best Local Similarity 30.2<sup>5</sup>
Matches 160; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                         Stone, David J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-004-378A-34
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November 10, 2004, 16:19:28 ; Search time 39 Seconds (without alignments) 1041.115 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-018-030B-2
2211
1 MAAASVTPPGSLELLQPGFS.....NSYVRDDAIFIKAIVDLTGL 422

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	or necrosis f	TNF receptor assoc	TNFR-associated pr	0 receptor-as	н	CD40 receptor-asso	٦,		MLN 62 protein - h	interl	ដ	dase	(EC 3.4	ination ac	A (EC 3.4	A (EC 3	A (EC 3	probable zinc-bind	transcription regu	ring finger B-box	meprin A (EC 3.4.2	in-related p	rot	ination-act	testis-abundant fi	pro	transforming prote	inger prote	PML-1 protein - hu
SUMMARIES	di	S56163	I61512	B55649	149272	A54750	S68467	A55960	JC6539	138026	871821	T22238	S24134	A48040	IS1055	A42908	HYHUMA	A40195	S28418	A57041	JC7753	HYHUMB	T14156	75	B33754	JC7387	T28734	TVHURE	TVHURF	A40044
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842517	S44381	A60198	B40045	S19244	A40045	S42518	S44382	T22363	S44380	842516	C40045	G84724	JC7562	A33754	149350
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113.5	113.5	113.5	113.5	113.5	113.5	113.5	113.5	113.5	113.5	113.5	113.5	112.5	112.5	112.5	112
30	31	35	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

 RESULT 1 SS6163
 tumor necrosis factor type 2 receptor associated protein - human N.Alternate names: TNF receptor-associated protein
 Cippecies: Nomo Saprens (man) Cibate: 10-0071-1995 #sequence_revision 01-Dec-1995 #text_change 09-Jul-2004 CiAccession: S56163; S58925; S58926; I38729 R;Song, H.Y.; Donner, D.B.
 Biochem. J. 309, 825-829, 1995 A;Title: Association of a RING finger protein with the cytoplasmic domain of the human ty A;Reference number: S56163; MUID:95366958; PMID:7639698
 A;Accession: S56163 A;Molcoule Type: mRNA A:Molcoule Type: mRNA
 A, Cross-references: UNIPROT:Q12933; EMBL:U12597; NID:g975272
 R.Song, H.Y.; Donner, D. subrary, July 1994 subtract to the EMBL Data Library, July 1994 submitted to the EMBL Data Library, July 1994
 SS8925
A;Accession: 538925 A;Molecule type: mRNA
A;Residues: 1-42,63-342,363-501 <50N2> A;Cross-references: EMBL:U12597; NID:g975272
A.Accesion: S58926
A;MOLECULE LYDE: MKNA A;Residues: 1-342,'RPFQAQCGHRYCSFCLASIL',363-501 <son3></son3>
A;Cross-references: EMBL:U12597; NID:g975272; PIDN:AAA87706.1; PID:g975273 P.Botha M . Wong S C . Wanzel W .T . Graddel D V
A;Title: A novel family of putative signal transducers associated with the cytoplasmic do A:Reference number: A54750; MUID:94349371; PMID:8069916
 A/Accession: 138729
 A;Schaus; preliminary; translated from GB/EMBL/DUBU A;Nolecule type: mRNA
 A;Residues: 1-342,'RPFQAQCGHRYCSFCLASIL',363-501 <rot></rot>
 Appropriate Control of the Control o
A;Gene: GDB:TRAF2; TRAP A:Tras reference: GDB.6268639: OMIM.601895
A, Map Dostlion: 9434-9634
C;Superfamily: TNF receptor-associated factor (TRAF); RING finger homology
C;Keywords: Zind Linger F;30-78/Domain: RING finger homology <rng></rng>
 tch 97.5%; Score 2156.5; DB 2; Length 501; al Similarity 84.0%; Pred. No. 3.5e-151;
 Marches 421; Conservative U; Mismarches I; Indels /9; Gaps I;
Db 1 MAAASVTPPGSLELLQPGFSKTLLGTKLEAKYLCSACRNVLRRPFQAQCGHRYCSFCLAS 60

QY 162 REHLAMLLSSVLEAKPLLGDQSHAGSELLQRCESLEKKTATFENIVCYLNREVERVAMTA 221 Db 241 REHLALLLSSFLEAQASPGTLNQVGPELLQRCGILEGKIATFENIVCYLNREVERVATA 300 222 EACSRQHRLDQDKIEALSSKVQQLERSIGLKDLAMADLEQKVLEMEASTYDGVFIWKISD 281	B55649 TMFR-associated protein EB16 - human C;Species: Homo sapiens (man) C;Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 09-Jul-2004 C;Accession: B55649 C;Accession: B55649 R;Mosialoso, G.; Birkenbach, M.; Yalamanchili, R.; VanArsdale, T.; Ware, C.; Kieff, E. R;Mosialoso, G.; Birkenbach, M.; Yalamanchili, R.; VanArsdale, T.; Ware, C.; Kieff, E. R;Mcference number: A55649; MUID:95163092; PMID:7859281 A;Reference number: A55649; MUID:95163092; PMID:7859281 A;Accession: B55649 A;Accession: B55649 A;Accession: B5649 A;Accession: Byeliminary A;Molecule type: mRNA A;Residues: I-416 < MNOS-A A;Cross-references: UNIPROT:013077; GB:U19261; NID:q675461; PIDN:AAA62309.1; PID:q675462	1 416; 1 83; Gaps 1 83; Gaps 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Qy 195SLEKKTATFENIVCVLNREVERVAMTAEACSRQHRLDQDKIEALSSKVQQLE 246 Db 181 FWKEKLLAELEGKLRVFENIVAVLNKEVEASHLALATSIHQSQLDRERILSLEQRVVELQ 240 Qy 247 RSIGLKDLAMADLEQKVLEMEASTYDGVFIWKISDFARKLQBAVGRIPAIFSPAFYTSR 306 C 1	QY 307 YGYKWCLRIYLNGDGTGRGTHLSLFPVVMKGPNDALLRWPFNQKVTLMLLDQNNREHVID 366 Db 301 YGYKLCLRLYLNGDGFGKRTHLSLFIVIMRGEYDALLPWPFRNKVTFMLLDQNNREHAID 360 QY 367 AFRPDVTSSSFQRPVNDMNIASGCPLFCPVSKMEA-KNSYVRDDAIFIKAIVD 418 Db 361 AFRPDLSSASFQRPQSETNVASGCPLFFPLSKLQSPKHAYVKDDTMFLKCIVE 413 RESULT 4 149272
	SGCPLFCPVSXMEA 40	C.Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004 C.Accession: 161312 R.Rothe, M.; Wong, S.C.; Henzel, W.J.; Goeddel, D.V. Cell 79, 681-692 1994 A.Title: A novel family of putative signal transducers associated with the cytoplasmic d A,Reference number: A54750; MUID:94349371; PMID:8069916 A,Accession: 161512 A,Accession: 161512 A,Accession: 161512 A,Reduce: preliminary; translated from GB/EMBL/DDBJ A,Reduce: preliminary; translated from GB/EMBL/DDBJ A,Residues: 1-501 cRES> A,Coross-references: UNIPROT:P39429; GB:L35303; NID:g532620; PIDN:AAC37662.1; PID:g532621 C,Genetics: A,Gene: TAKR2 C,Genetics: A,Gene: TAKR2 C,Superfamily: TNF receptor-associated factor (TRAF); RING finger homology C,Reywords: Zinc F;30-78/Domain: RING finger homology cRNG>	Query Match 86.6%; Score 1914.5; DB 2; Length 501; Best Local Similarity 74.3%; Pred. No. 2.4e-133; Added: 372; Added: 372; Conservative 21; Mismatches 29; Indels 79; Gaps 1; Qy 1 MAAASVTEPGSLELLQPGFSKTLLGTKLEAKYLCSACRNLRRPFQAQCGHRYCSFCLAS 60 Db 1 MAAASVTSPGSLELLQPGFSKTLLGTRLEAKYLCSACRNLLRRPFQAQCGHRYCSFCLTS 60	OY 61 ILSSGPONCAACVHEGIYEEGISILESSSAFPDNAARREVESLPAVCPSDGCTWKGTLKE 120

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Codoreceptor-associated protein CAP-1 - human Cispecies: Homo sapiens (man) Cispecies: Juli-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004 Ciscossion: S68467, IS3498, J.C. FERS Lett.: S186, Ill-3-118, 1995 A: Read, J.C. FERS Lett.: S186, Ill-3-118, 1995 A: Reference number: IS3498, MUID:95129692; PMID:7530216 A: Accession: S68467 A: Accession: S68467 A: Residues: I-543 csdrs: mana A: Residues: I-543 csdrs: MIDROT:Q13114; EMBL:L38509; NID:g695357; PIDN:AAA68195.1; PID:g69538 A: Experimental source: tissue-type fetal brain Cigenetics:
                                             A,Accession: A54750
A,Status: prellmary: translated from GB/EMBL/DDBJ
A,Kotacule type: mRNA
A,Residues: 1-409 <RES>
A,Cross-references: UNIPROT:P39428; GB:L35302; NID:g532618; PIDN:AAC37663.1; PID:g532619
C,Genetics:
A,Gene: TRAF1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            119 WKSSPGSNLGSAPMALERNLSELQLQAAVBATGDLEVDCYRAPCCESQEELALQHLVKEK 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                179 LLAQLEEKLRVFANIVAVLNKEVEASHLALAASIHQSQLDREHLLSLEQRVVELQQTLAQ 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      299 CLRLYLNGDGSGKKTHLSLFIVIMRGEYDALLPWPFRNKVTFMLLDQNNREHAIDAFRPD 358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59 VSPGSPLTQEKVHSDVAEAEIMCPFAGVGCSFKGSPQSMQEHEATSQSSHLYLLLAVLKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               196 ----LEXKTATFENIVCVLNREVERVAMTAEACSROHRLDODKIEALSSKVQQLERSIGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Gene: CAP-1
C,Superfamily: TNF receptor-associated factor (TRAF); RING finger homology
C;Keywords: homodimer; signal transduction; zinc finger
F,49-97/Domain: RING finger homology <RNG>
                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85 LESSSAFPDNAARREVESLPAVCPSDG----CTWKGTLKEYEFQDHVKTCGKCR-
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llarity 34.9%; Pred. No. 1.8e-45;
Conservative 77; Mismatches 124; Indels 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               359 LSSASFQRPQSETNVASGCPLFFPLSKLQSPKHAYVKDDTMFLKCIVD 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      372 VISSSFØRPVNDMNIASGCPLFCPVSKMEA-KNSYVRDDAIFIKAIVD 418
                                                                                                                                                                                                                                                                                                                                                               Length 409;
                                                                                                                                                                                                                                                                                                                                                       tch 32.9%; Score 727; DB 2; Length 40: al Similarity 38.5%; Pred. No. 5.4e-46; 157; Conservative 63; Mismatches 112; Indels
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        A; Reference number: A54750; MUID: 94349371; PMID: 8069916
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Best Local S:
Matches 184
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Best Local S:
Matches 157
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CD40 receptor-associated factor 1 - mouse
C.Species: Mus musculus (house mouse)
C.Species: Mus musculus (house mouse)
C.Species: Mus musculus (house mouse)
C.Accesaion: 199272
R.Cheng, G.; Cleary, A.M.; Ye, Z.S.; Hong, D.I.; Lederman, S.; Baltimore, D. Science 267, 1494-1498, 1995
A.Title: Involvement of CRAFI, a relative of TRAF, in CD40 signaling.
A.Tatle: Involvement of CRAFI, a relative of TRAF, in CD40 signaling.
A.Reference number: A55960; MUID:95184010; PMID:7533327
A.Status: Preliminary
A.Molecule type: mRNA
A.Residues: 1-567 «RES>
A.Cross-references: UNIPROT:Q60803; EMBL:U21050; NID:g719292; PIDN:AAC52175.1; PID:g7192
C.Genetics:
A.Gene: CRAFI
C.Superfamily: TNF receptor-associated factor (TRAF); RING finger homology
C.Reywords: zinc finger
F;48-96/Domain: RING finger homology «RNG»
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A54750

A54750

Disperies: Mus musculus (house mouse)

C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004

C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004

C;Accession: A54750

C;Accession: A54750

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C;Accession: A54750

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C;Accession: A54750

A;Title: A novel family of putative signal transducers associated with the cytoplasmic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MAAASVTPPGSLELLQP-----GFSKTLLGTKLEAKYLCSACRNVLRRPPQA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 33.0%; Score 730; DB 2; Length 567; Similarity 32.1%; Pred. No. 4.9e-46; Conservative 80; Mismatches 131; Indels 184;
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Best Local Simi
Matches 187;
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дG	:: : : : :	Best Local Matches 1	cal Similarity 33.2%; Pred. No. 4.1e-45; 184; Conservative 75; Mismatches 124; Indels 171; Gaps 22;
oy.	119CRFHAIGC- 144 116 LPCVRPDCKEKVLRKDLRDHVEKACKYREATCSHCKSQVPMIALQKHEDTDCPCVVVSCP 205	ç qa	16 OPGESKTLLGTKLEAKYLCSACRNVLRRPPQAQCGHRYCSFCLASILSSGPQNCAACVHE 75 1
oy. Dp	145LETVEGEKQQEHEVQWIREHLAMLLSSVLEAKPLIGDQSHAGSELLQRC 193 206 HKCSVQTLLRSEGTNQQIKAHEASSAVQHVNLLKEWSNSLEKKVSLLQN- 254	QJ QD	76 GIYEEGISILESSSAFPDNAARREVESLPAVCPSDGCTWKGTL 118
oy Q	194 ESLEKKTATFENIVCVLNREVERVAMTAEACS 225 : : : : : : 255 ESVEKNKSIQSLHNQICSFEIEIERQKEMLRNNESKILHLQRVIDSQAEKLKELDXEIRS 314	ç ç	119
& ସ	226 -RQHRLDQDKIEALSSKVQQLERSIGLKDLAM 256 : : : : : : : 313 FRQNWEEADSMKSSVESLQNRVTELESVDKSAGQVARNTGLLESQLSRHDQMLSVHDIRL 374	<u>ئ</u> ۾	137
S S	257 ADLEQKVLEMEASTYDGVFIWKISDFARKLQEAVAGRIPAIFSPAFYTSRYGYRMCLRIY 316 :::	රු දි	169LSSVLBAKPLLGDQSHAGSELLQRCESLEKKTATPENIVCVLNREVER 216
δ. O.	317 INGDGTGRGTHLSLFFVVMKGFNDALLRWPFNQKVTLMLLDQ-NNREHVIDAFRPDVTSS 375	65 62	217VAMTAEACS
oy O	376 SFORPVNDMMIASGCPLFCPVSKWFAKNSYVRDDAIFIKAIVDLIGL 422 :: : : : : :	oy Dp	247RSIGLKDLAMADLEGKVLEMEASTYDGVFINKISDFARKLQEA 289 :
		දු පු	290 VAGRIPAIFSPAFYTSRYGYKWCLRIYLNGDGTGRGTHLSLFFVVMKGPNDALLRWPFNQ 349
CD40 recep N,Alternat C,Species: C,Date: 15	receptor-associated factor 1 - human ernate names: CD40-binding protein cies: Homo sapiens (man) e: 15-Mar-1996 #sequence_revision 15-Mar-1996 #text_change 09-Ju1-2004	<i>&</i> 43	350 KVTLMLLDQ-NNREHVIDAFRPDVTSSSFQRFVNDMNIASGCPLFCFVSKMEAKNSYVRD 408
C,Accessic R,Cheng, C Science 26 A,Title: I	CjAccession: ASSB01, ASSB49; ASSL35 R;Chang, G.; Cleary, A.N.; Ye, Z.S.; Hong, D.I.; Lederman, S.; Baltimore, D. Science 267, 1494-1498, 1995 A;Title: Involvement of CRAFI, a relative of TRAF, in CD40 signaling.	co Op	409 DAIFIKAIVDLTGL 422 : 552 DIFIKVIVDTSDL 565
A; Kererenc A; Accessic A; Status:	ce number: Abbybo; MUID:95184010; FMID:753327 nn: Abb960 treliminary tree: mbwn	RESULT 8	
A; Residues A; Cross-re R; Mosialos	3: 1-568 <regs 2: 1-568 <regs 2: 1-568 <regs: embl:u21092;="" nid:g726087;="" pid:g7260<br="" pidn:aac50112.1;="" uniprot:q13114;="">3: G.; Birkenbach, M.; Yalamanchili, R.; VanArsdale, T.; Ware, C.; Kieff, E.</regs:></regs </regs 	tumor neci C,Species C,Date: 05	crosis factor receptor-associated factor 5 homolog - human ss: Homo sapiens (man) 05-Dec-1938 #sequence_revision 05-Dec-1998 #text_change 09-Jul-2004
Cell 80, : A;Title: T A;Referenc A;Accessio	889-399, 1995 Re Epstein-Barr virus transforming protein LMP1 engages signaling proteins for Pe number: A55649; MUID:95163092; PMID:7859281 pn: A55649	C, Accessic R, Mizushin Gene 207, A, Title: (nn: UC653F 135-140, 1998 135-140, 1998 Noning and characterization of a cDNA encoding the human homolog of tumor necro
A;Status: A;Molecule A;Residues		A;Referenc A;Accessic A;Molecule	ID:9511754
A, Cross-re R, Hu, H.M. J. Biol. C A, Title: A	A,Cross-references: GB:UJ9260; NID:g675459; PIDN:AAA65732.1; PID:g675460 R;Hu, H.M.; O'Rourke, K.; Boguski, M.S.; Dixit, V.M. J. Biol. Chem. 269, 30069-30072, 1994 A;Title: A novel RING finger protein interacts with the cytoplasmic domain of CD40.	A; Residues A; Cross-re C; Comment: mphotoxin-	A;Residues: 1-557 <miz> A;Cross-references: UNIPROT:000463; DDBJ;AB000509; NID:g2982670; PIDN:BAA25262.1; PID:g25 C;Comment: This protein is involved in transduction of signals from various tumor necrosi mphotoxin-beta receptor.</miz>
A; Kererenc A; Accessic A; Status: A; Molecule A; Residues	se number: Absiss; MulD:950/3988; PMID:/52/023 nn: Absiss nucleic acid sequence not shown : 1-128.7 W.,130-133,135-404,'G',406-568 https://doi.org/10.133.135-404 , 'G',406-568 https://doi.org/10.133.135-404 , 'G',406-568 https://doi.org/10.133.135-404 , 'G', '406-568	C, Genetics: A, Map position: C, Superfamily: TR C, Keywords: coile F:41-90/Domain: R	Genetics: 1932.3-1941.1 Map position: 1932.3-1941.1 Superfamily: TNF receptor-associated factor (TRAF); RING finger homology Keywords: colled coli; tumor; Zinc finger 41-90/Domain: RING finger homology «RRN»
A;Cross-re C;Genetics A;Gene: CR C;Superfam	A;Cross-references: GB:U15637; NID:g595910; PIDN:AAA56753.1; PID:g595911 C;Genetics: A;Gene: CRAF1 C;Superfamily: TNF receptor-associated factor (TRAF); RING finger homology	Query Match Best Local S Matches 160	31.1%; Scc llarity 30.2%; Pre Conservative 85;
F;49-97/Do	•	ò ;	KLEAKYLGSACRNVLRRPFGAQCGHRYCSFCLASILSSGPONCAACVHEGIYEEGISI
Query Match	ltch 32.5%; Score 717.5; DB 2; Length 568;	q a .	38 RLEERYKCAFCHSVLHNPHQTGCGHRFCQHCILSLRELNTVPICPVDKEV 87

99 INSSSAPPDNAMARRYESLPANCP-SDCTWKGTILKEY-CONLOCLEPOYCESNERGE 90 INSOCREPRONCCERPINITYCENAPOCHANTICARY-CONLOCLEPOYCESNERGE 91 INSOCREPATION CONTROLLER C
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A48040
meprin A (EC 3.4.24.18) beta chain precursor - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jun-1995 #sequence_revision 02-Jun-1995 #text_change 17-Feb-2003
C;Accession: A48040
R;Gorbea, C.M.; Marchand, P.; Jiang, W.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.; Bc
J. Biol. Chem. 268, 21035-21043, 1993
A;Title: Cloning, expression, and chromosomal localization of the mouse meprin beta subur
A;Reference number: A48040
A;Accession: A48040
A;Accession: A48040
A;Residues: preliminary
A;Molecule type: mRNA
A;Residues: 1-704 GGR>
A;Cross-references: GB:L15193
C;Superfamily: meprin; astacin homology; EGF homology; MAM homology
C;Reywords: hydrolase; metalloproteinase; zinc
C;Superfamily: meprin; astacin homology cAST>
F;72-258/Domain: BGF homology cAST>
F;611-646/Domain: EGF homology cAGF>
F;611-646/Domain: EGF homology cAGF>
F;153,157,163,212/Binding site: zinc (His, His, Tyr) #status predicted
F;154/Active site: Glu #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ricorbeil, D.; Gaudoux, F.; Wainwright, S.; Ingram, J.; Kenny, A.J.; Boileau, G.; Crine, PEBS Lett. 309, 203-208, 1992
A;Title: Molecular cloning of the alpha-subunit of rat endopeptidase-24.18 (endopeptidase A;Reference number: S24114; MUID:92271675; PMID:1505684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A Status: preliminary
A Modecule type: mRNA
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A MODECULE TYPE CONTROL TO THE CONTROL TYPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          493 SGDNDVILEWPVENEQAIMTILDQEPDARNRMSLSLMF----TTSKYQTSSAINGSVIWD 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    276 IWKISDFARKLQEAVAGRIPAIFSPAFYTSRYGYKMCLRIYLNGDGTGRGTHLSLFFVVM 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            436 VWTIRNISQVLENTVKG--DRLVSPRFYNSE-GYGFGVTLYPNGRITSNSGYLGLAFHLY 492
                                                                                                                                                                                                                                                                                                                                                                                          Species: Rattus norvegicus (Norway rat)
.Date: 02-Dec-1993 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6.3%; Score 139; DB 2; Length 748; 27.0%; Pred. No. 0.023; tive 26; Mismatches 67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 6.1%; Score 135; DB 2; Length 704; Best Local Similarity 25.9%; Pred. No. 0.043; Matches 45; Conservative 35; Mismatches 54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            336 KGPNDALLRWPF-NOKVTLMLLDQ----NNREHVIDAFRPDVTSSSFQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;265-434/Domain: MAM homology <MAM>
F;765-111/Domain: EGF homology <EGF>
F;165,160,166/Binding site: Zinc (His) #status predicted
F;157/Active site: Glu #status predicted
                                                                                                                                                                                                                                                                                                        endopeptidase 2 (EC 3.4.24.-) - rat
N;Alternate names: endopeptidase 24.18
                                                  : :||:|| | ::: | | 444 Q---NYVKDDKIYVQIDVD 459
    400 EAKNSYVRDDAIFIKAIVD 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 47; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Accession: S24134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: S24134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Accession: T22238
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Mosicuse: 1-509 <WIL>
A;Kesiduse: 1-509 <WIL>
A;Cross-references: UNIPROT:062248; EMBL:293382; PIDN:CAB07615.1; GSPDB:GN00021; CESP:F4
A;Experimental source: clone F4562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Map position: 3
A;Introns: 94/2; 119/3; 201/3; 223/3; 249/1; 277/3; 300/3; 327/3; 360/1; 395/3; 448/3
C;Superfamily: TNF receptor-associated factor (TRAF); RING finger homology
F;61-107/Domain: RING finger homology <RRN>
                                                                                                                                                                                                                                                                                                        ERSIGLKDLAMADLEOKVLEMEASTYDGVFIWKISDFARKLQEAVAGRIPAIFSPAFYTS 305
                                                                                                                                                                                                                                                                                                                                                                                                                         306 RYGYKMCLRIYLNGDGTGR-GTHLSLFFVVMKGPNDALLRWPFNQKVTLMLLDQN---- 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                384 KPGYKLCMRLHLOLPTAQRCANYISLFVHTMQGEYDSHLPWPFQGTIRLTILDQSEAPVR 443
LDCPTAPIPCTFSTFGCHEKMQRNHLARHLQENTQSHMRMLAQPV-HSLSVIPDSGYI-- 289
                                                                                                                                                               ---SEVRNPOETIHOLEGRLVR------QDHQIRELTAKMETQSMYVSEL 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      360 -WREHVIDAFRPDVTSSSFQRPVNDMNIAS-GCPLFCPVSKMEAKNSYVRDDAIFIKAIV 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SSAFPDNAARREVESLPAVC--PSDGCTWKGT-----LKEYEFQDHVKTCGKC---- 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | | :::: :|| || | | || || || ELCQHDRAKQKQILALPVVCTFESSGCPWDGQLGTLHDHLSECTFKSSLK-CEKCGRQFA 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ------RVPCRFHAIGCLETVEGEKQOEHEVQWLREHLAMILSSVLEAKPLL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       167 KNDLEKHRAKCELNRAVCSF----CNKTIRDSDRERHPKTCPQVIISCPFQCGLTDRPRL 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       223 BIEAHCPS-----QPNVD-NVCPFVPYGCTFAGGKESI------QQHLSDEPVRHLMY 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LPADCTCPICEQALRDPIKINCDHHYCRQCFEN--ENRIPGCAACQ-----TIIQP 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --DKIEALSSKVQQLERSIGLKDLAMADLEQKVLEMEASTYDGVF----IWKISDFARKL 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QEAVAGRIPALFSPAFYTSRYGYKMCLRIYLNGDGTGRGTHLSLFFVVMKGPNDALLRWP 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FNOKVTLMLLDQN-----NREHVIDAFRPDVTSSSFORPVNDMNIASGCPLFCPVSKM 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein F45G2.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T22238
R;Lindsay, S.
Submitted to the EMBL Data Library, March 1997
                                                                                 188 ELLORCESLEKKTATFENIVCVLNREVERVAMTAEACSROHRLDO--DKIEALSSKVOOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28 LEAKYLCSACRNVLRRPFQAQCGHRYCSFCLASILSSGPQNCAACVHEGIYEEGISILES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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; Pred. No. 2e-21;
65; Mismatches 171; Indels
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Best Local Similarity 26.7%;
Matches 117; Conservative 6
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Gene: CESP:F45G2.6
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Gaps

49;

DB 1; Length 668; Indels

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C;Accession: A42908
R;Acression: A42908
R;Ajohnson, G.D.; Hersh, L.B.
R;Johnson, G.D.; Hersh, L.B.
R;Aile: Cloning a rat meprin cDNA reveals the enzyme is a heterodimer.
A;Title: Cloning a rat meprin cDNA reveals the enzyme is a heterodimer.
A;Reference number: A42908; MUD:92317075; PMID:1377685
A;Accession: A42908
A;Accession: A42908
A;Molecule type: mRNA
A;Residues: 1-668 aJOH>
A;Molecule type: mRNA
A;Residues: 1-668 aJOH>
A;Cross-references: UNIPROT:P28826
A;Note: sequence extracted from NCBI backbone (NCBIP:107784)
C;Superfamily: meprin; astacin homology; EGF homology; MAM homology
C;Reywords: heterodimer; hydrolase; metalloproteinase; zinc
F;72-258/Domain: mAM homology aAST>
F;261-430/Domain: MAM homology aAST>
F;561-430/Domain: MAM homology and AMST P;153,157,163,212/Binding site: zinc
F;153,157,163,212/Binding site: zinc
F;154/Active site: Glu #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         276 IWKISDFARKLQEAVAGRIPAIFSPAFYTSRYGYKMCLRIYLNGDGTGRGTHLSLFFVVM 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       432 İWHIQNFTQLL----GGQTTVYSPPFYSSK-GYAFQINLDLTSP----TNVGLYFHLI 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 365 IDAFRPDVISSSFQRPVNDMNIASGCPLFCPVSKMEAKNSYVRDDAIFIKAIVDLIGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.0%; Score 132.5; DB 1;
24.2%; Pred. No. 0.061;
tive 31; Mismatches 55;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Oncorhynchus mykiss (rainbow trout)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: 151055
R;Hansen, J.D.; Kaattari, S.L.
Immunogenetics 42, 188-195, 1995
A;Title: The recombination activation gene 1 (RAG1) of rainbow trout (Oncorhynchus mykis A;Reference number: 151055; MUID:95369845; PMID:764230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: DNA
A;Residues: 1-1073 <HAN>
A;Cross-references: UNIPROT:Q91187; EMBL:U15663; NID:g558917; PIDN:AAA80281.1; PID:g5589
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21;
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          IWKISDFARKLQEAVAGRIPAIFSPAFYTSRYGYKMCLRIYLNGDGTGRGTHLSLFFVVM 335
                                           380
                                                                                                                                                              482 SGANDDOLOWPCPWOOATMTLLDONPDIRORMFNORSITTD---FTMTSDNGSYFWDRPS 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SARLLSEDLPVDFLSSVTCQVCDHLLSEPVQSPCRHLFCRSCIAKYIYSLGP-HCPACT- 349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             243 QQLERSIGLKDLAMADLEQKVLEMEASTYDGVFIWKISDFARKLQEAVAGRIFAIFSPAF 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---GRGFGLHPAVCLAIRVNTF-LSCSQYHKMY-----RTVKATSGR--QIFQP-L 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  303 YTSRYGYKMCLRIY-----LNGDGTGRGTHLSLFFVVMKGPNDALLRWPFNQKVTLM 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      533 HTLRTAEKELLPGYHPFEWQPALKSVST--SCHVGII------DGLSGW-----IA 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74
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                                                                                                                                                                                                               ---VNDM-----NIASGCPLFCPVSKMEAKNSYVRDDAIFIKAIVDLTGL 422
                                                                                                                                                                                                                                                                539 KVGVTDVFPNGTQFSRGIGYGTTVFITRERLKSREFIKGDDIYILLTVEDISHL 592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.0%; Score 133.5; DB 2; Length 1073; 22.2%; Pred. No. 0.092;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45; Mismatches 148;
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                                                                                                                                                                                                                                                                                                                                               RESULT 14
151055
recombination activating protein - rainbow trout
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A;Gene: RAG-1
A;Introns: 489/1
C;Keywords: 2inc
F;306-354/Domain: RING finger homology <RNG>
                                                                                                             336 KGPNDALLRWPFN-QKVTLMLLDQ
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Matches 84; Conser
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85 ILSSGPQNCAACVHEGIXEEGISILESSSAFPDNAARREVESLPAVCPSDGCTWKGTLKE
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Q7Z337
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Q12933 homo sapien
Aat64662 homo sapi
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                                                                                                                                       November 10, 2004, 16:11:42 ; Search time 195 Seconds (without alignments) 1245.170 Million cell updates/sec
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                                                                                                                                                                                                                                               US-10-018-030B-2
2211
1 MAAASVTPPGSLELLQPGFS......NSYVRDDAIFIKAIVDLTGL
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
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TRA4 HUMAN
Q6DFG9
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AAH64662
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Maximum Match 100%
Listing first 45 summaries
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Q90WT6
Q6NRN3
AAH70713
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Q6DEV2
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
2: uniprot_trembl:*
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Maximum DB seq length: 200000000
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Match Length DB
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1914.5
1914.5
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1149.5
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1131.5
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430.5
430.5
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No.
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Aah60705 mus muscu

Q8quj9 infectious

P70196 mus musculu

Q6djn2 xenopus lae

Q94X8 homo sapien

Q951x1 macaca fasc

Q75xx1 brachydanio

Q61u1 brachydanio

Q61u14 brachydanio

Q61u14 brachydanio

Aat37634 Brachydanio

Q7pxx7 anopheles g

Q7q116 anopheles g
   mus musculu
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A Ottenwaelder B., Obermaier B., Deutschenbaur S., Mewes H.W., Weill

A Ottenwaelder B., Obermaier B., Deutschenbaur S., Mewes H.W., Weill

A Mid C., Osanger A., Fobo G., Han M., Wiemann S.;

Submitted (JUN-2003) to the BMEL/GenBank/DDEJ databases.

C. -1 SIMILARITY: Contains I RING-type zinc finger.

EMBL, BX538160; CAD98040.1;

EMBL, BX538160; CAD98040.1;

GO; GO:0000151; C:ubiquitin-protein ligase activity; IEA.

GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.

GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.

GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.

R GO; GO:0008270; F:zinc ion binding; IEA.

R GO; GO:0016567; F:zinc ion binding; IEA.

R FFam; PRO017; MATH; 1.

R FFam; PRO017; MATH; 1.

R FFAM; PRO017; AFAF; 1.

R RART; SM00164; MATH; 1.

R PROSITE; PS00164; MATH; 1.

R PROSITE; PS00164; MATH; 1.

R PROSITE; PS00149; ZE_RING_2; 1.

R PROSITE; PS00149; ZE_RING_2; 1.

M PROSITE; PS00145; ZE_RRAF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Name-DFYZD686H1465;
Name-DFYZD686H1465;
Homo saplens (Human)
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88.4%; Pred. No. 1.5e-144;
ive 0; Mismatches 1;
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Q6P9M0
AAH6070S
Q8QUJ9
TRA6 MOUSE
G6DJN2
Q95LR1
Q75XX1
Q95LR1
Q75XX1
Q61W4
AAT37634
Q72116
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Best Local Similarity 88.4'
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    NCBI_TaxID=9606;
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307 YGYKMCLRIYLNGDGTGRGTHLSLFFVVMKGPNDALLRWPFNQKVTLMLLDQNNREHVID 366
                                      127 VKTCGKCRVPCRFHAIGCLETVEGEKQQEHEVQWLREHLAMILSSVLEAKPLLGDQSHAG 186
                                                                                                                                                                                   RSIGLKDLAMADLEQKVLEMEASTYDGVFIWKISDFARKRQEAVAGRIPAIFSPAFYTSR 384
                                                                                                                       SELLQRCESLEKKTATFENIVCVLNREVERVAMTAEACSRQHRLDQDKIEALSSKVQQLE 324
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We pubmed=14702039; DOI=10.1038/ng1285;

Pubmed=14702039; DOI=10.1038/ng1285;

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Bekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,

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Bajahari K., Murakami K., Yasuda T., Iwayanagi T., Rikkawa E.,

Romira Y., Abdo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,

Sugawara M., Takahashi M., Kanihara K., Yokoi T., Furuya T., Kitkawa E.,

Omura Y., Abe K., Kanihara K., Ishibashi T., Yamashita H., Murakawa K.,

Pujimori K., Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y.,

Rusano J., Kanehori K., Takahashi-Pujii A., Hara H., Tanase T.-O.,

Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M.,

Imose N., Musashino K., Yuuki H., Oshima A., Sasaki N., Aoteuka S.,

Moriya S., Momiyama H., Satoh N., Takami S., Takeuchi K., Wakebe H.,

Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shinizu F., Nawakami B.,

Yamazaki M., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,

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Kamazaki M., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,

Yamazaki M., Watanabe T., Kobatake N., Ikana M., Ohmori Y.,

Kawabata A., Hikiji T., Kobatake N., Itana M., Ohmori Y.,

Kawabata A., Hikiji T., Kobatake N., Itana M., Sasaki M.,

A Ono T., Yamada X., Natuno T., Morinaga M., Sasaki M.,

Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
         145 YESCHEGRCPLMLTECPACKGLVRLGEKERHLEHECPERSLSCRHCRAPCCGADVKFODH 204
                                                             205 VKTCGKCRVPCRFHAIGCLETVEGEKQQEHEVQWLREHLAMLLSSVLEAKPLLGDQSHAG
                                                                                                                                                              RSIGLKDLAMADLEQKVLEMEASTYDGVFIWKISDFARKLQEAVAGRIPAIFSPAFYTSR
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                                                                                                    SELLORCESLEKKTATFENIVCVLNREVERVAMTAEACSROHRLDODKIEALSSKVOOLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=95366958; PubMed=7639698; Song H.Y., Donner D.B.; Association of a RING finger protein with the cytoplasmic domain of the human type-2 tumour necrosis factor receptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Name=TRAF2; Synonyms=TRAP3;
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RELIBES 2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.D., Feingold B.A., Grouse L.H., Derge J.G.

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Diatchenko L., Marusina K., Farmer A.H., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.H., Rubin G.M., Hong L.,

READ Exchaefer M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Millahy S.J.,

Rosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Rosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Hilalon D.K., Muzuy D.W., Sodergren B.J., Lu X., Gibbs R.A.,

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Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

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R. Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;

R. Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-96195221, PubMed-8627180,

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the CD30 cytoplasmic domain in association with tumor necrosis factor

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INTERACTION WITH INFRSF14.
MEDLINE=97298041; PubMed=9153189;
MEDLINE=97298041; PubMed=9153189;
MEDLINE=97298041; Colombero A., Elliott R., Kelley M., Boyle W.J.;
"ATAR, a novel tumor necrosis factor receptor family member, signals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=94349371; PubMed=8069916; Rothe M., Wong S.C., Henzel W.J., Goeddel D.V.; An ovel family of putative signal transducers associated with the cytoplasmic domain of the 75 kDa tumor necrosis factor receptor."; Cell 78:681-692(1994).
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Wajant H., Henkler F., Scheurich P.;
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Rothe M., Xiong J., Shu H.-B., Williamson K., Goddard A.,
Goeddel D.V.;
"I-TRAF is a novel TRAF interacting protein that regulates TRAF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 201-501 FROM N.A., AND INTERACTIONS WITH TRAF1 AND
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DOI=10.1002/(SICI)1521-4141(199807)28:07<2208::AID-IMMU2208>3.0.CO;2-L;
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                                    INTERACTION WITH TRIP.

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through TRAF2 & J. Biol. Chem. [10]
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TISSUB-Uterus;

TISSUB-Uterus;

Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Straubberg R.L., Zeberge B., Wagner L., Shemmen C.M., Schuler G.D.,

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Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                INTERACTION WITH MAP3KS.
MEDLINE=98448103; PubMed=9774977;
Nishitoh H., Saitoh M., Mochida Y., Takeda K., Nakano H., Rothe
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02-WAR-2004 (TrEMBLrel. 27, Last sequence update)
02-WAR-2004 (TrEMBLrel. 27, Last annotation update)
TNF receptor-associated factor 2, isoform 1.
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"CD28-independent, TRAF2-dependent 4-1BB ligand."; J. Exp. Med. 187:1849-1862(1998).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC064662; AAH64662.1; -.
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AAT27320;
01-JUN-2004 (TrEMBLrel. 27, Created)
01-JUN-2004 (TrEMBLrel. 27, Last sequence update)
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TNF receptor-associated factor 2.
                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
VCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match

97.5%; Score 2155.5; DB 2; Length 501;
Best Local Similarity 84.0%; Pred. No. 1.2e-143;
Matches 421; Conservative 0; Mismatches 1; Indels 79;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                     SEQUENCE FROM N.A.
Rieder M.J., Daniels R.L., da Ponte S.H., Hastings N.C., is ajkumar N., Yi Q., Nickerson D.A.;
Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AY623660; AAT27320.1; -.
                                                                                                                                                                                                                                                                                                                                                                   501 AA; 55859 MW; C508BE185B783B20 CRC64;
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AC 979429; 054896; DT 01-FEB-1995 (Rel. 31, Careated)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-DT-2004 (Rel. 45, Last annotation update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE TNF receptor associated factor 2.
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PROJECTOR STORY NA. (18070RW 2).

REMINING STROWN STRO
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CHESTORY (WE SIMILARITY) (WE SIMILARITY).

THEREPLY (WE SIMILARITY) (WE SIMILARITY).

ANGOLIAGES WITH PITTERS (WITH STREET AND THREETS (MORE))

ANGOLIAGES WITH PITTERS (WITH STREETS (MORE)).

THEREPLY (WE SIMILARITY).

THEREPLY (WE SIMI
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us-10-018-030b-2.rup

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SEQUENCE FROM N.A.
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01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Mus musculus 16 days neonate heart cDNA, RIKEN full-length enriched
library, clone:D830048Al0 product:Inf receptor-associated factor 2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                             79;
                                                                                                                                                                       DB 1; Length 501;
                                                                                                                                                                                         74.3%; Pred. No. 1.2e-126; ive 21; Mismatches 29; Indels
                                                                                           L -> LRCASILS (in isoform 2)
/FTId=VSP 007402.
043B391180365F10 CRC64;
RING-type.
TRAF-type 1.
TRAF-type 2.
Coiled coil (Potential).
MATH.
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MEDINE=99279253; Pubmed=10349636;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
"High-efficiency full-length cDNA (1999).
[2]
                                                                                                                                                                       Score 1914.5;
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                                                                                                                               501 AA;
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SEQUENCE FROM N.A.
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ZN_FING
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DOMAIN
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AC Q8C6X9
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D2 01-M
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D4 01-M
D5 01-M
D6 01-M
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SEQUENCE FROM N.A.

SIRAIN=C57BL/6J; TISSUB=Heart;
Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
Adachi J., Aizawa K., Akimura T., Hara A., Hashizume W.,
Antuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
Antuda S., Furuno M., Hiramoto K., Hiraoka T., Hirozane T.,
Antuda K., Ishini Y., Itoh M., Kagawa I., Kasukawa T.,
Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M.,
Katoh H., Kawai J., Kojima Y., Condo M., Nakamura M.,
Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Oksazki Y.,
Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
Tagawa A., Takahashi F., Takaku-Akahira S., Takada Y., Tanaka T.,
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
SIMILARITY: Contains I RING-type zinc finger.
BEMBI, AKOS2934; BAC3S2091; -.
                                                                                                                                                                                                                                                                                                                                           The FANTOM Consortium, the RIKEN Genome Exploration Research Group Phase I & II Team; the RIKEN Genome Exploration Research Group Phase I & II Team; Manalysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=CS/BL/6J; TISSUE=Heart,
MEDLINE=20499374; PubMed=11042159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
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MEDLINE=CSTBL/GG TISSUE=Heart;

MEDLINE=CSTBL/GG TISSUE=Heart;

MEDLINE=CSTBL/GG TISSUE=Heart;

MEDLINE=CSTBL/GG TISSUE=Heart;

Konno H., Akiyama M., Mishi K., Kitsunai T., Tashiro H., Itoh M.,

Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

Sumannoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,

Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,

"RIKEN Integrated sequence analysis (RISA) system-384-format

sequencing pipeline with 384 multicapillary sequencer.";
                                                                                              RIKEN FANTOM Consortium; "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R GO; GO:000151, C:ubiquitin ligase complex; IEA.

R GO; GO:000151, C:ubiquitin ligase complex; IEA.

R GO; GO:0004872; F:receptor activity; IEA.

GO; GO:0008270; F:rainc ion binding; IEA.

R GO; GO:0008270; F:rainc ion binding; IEA.

R GO; GO:001657; P:protein ubiquitination; IEA.

R InterPro; IPR002083; MATH.

R InterPro; IPR001293; Znf_TRAF.

R InterPro; IPR001293; Znf_TRAF.

R Ffam; PF0097; Zf-C3HC4; 1.

R Ffam; PF0097; Zf-C3HC4; 1.

R SMART; SM00184; RING; 1.
STRAIN=C57BL/6J; TISSUE=Heart;
MEDLINE=21085660; PubMed=11217851;
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PROSITE; PS00518; ZF RING 1; 1.
PROSITE; PS50089; ZF RING 2; 1.
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STRAIN=C57BL/6J; TISSUE=Heart;
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SEQUENCE FROM N.A.
STRAIN=CS7BL/6J; IISSUE=Thymus;
The FANTOM CONSORTIUM,
The RANTOM GONSORTIUM,
The RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
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 Nature 409:685-690(2001)
                                                                                                                     Nature 420:563-573(2002)
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Mus musculus 16 days neonate thymus cDNA, RIKEN full-length enriched
library, clone:Al30081B14 product:Tnf receptor-associated factor 2,
full insert sequence.
Musculus Traft;
                                                                                        Gaps
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Wakaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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STRAINE-SCYBL/6J, TISSUE-Thymus,
MEDLINE-2108-660; Fubmed-11217851;
RIKEN FANYOM CONSORTium,
"Functional annotation of a full-length mouse cDNA collection.";
                                                                                        79;
                                                            2; Length 501;
                                                                                       Indels
PROSITE; PS50145; ZF TRAF; 2.
Metal-binding; RecepTor; Zinc; Zinc-finger.
SEQUENCE 501 AA; 56086 MW; 89DDCB177B2BBF1F CRC64;
                                                          Query Match

86.6%; Score 1914.5; DB 2;
Best Local Similarity 74.3%; Pred. No. 1.2e-126;
Matches 372; Conservative 21; Mismatches 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=CS7BL/6J; TISSUE=Thymus;
MEDLINE=99279253; Pubmed=10349636;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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REAUNCE FROM N.A.

REAGUINGE FROM N.A.

REAGUINGE TO Alzawa K., Atlamura T., Arakawa T., Bono H., Carninci P., Adadawi J., Alzawa K., Atlamura T., Arakawa T., Harbizume W., Alzawa K., Atlamura T., Hara A., Hashizume W., RA Hayashida K., Hayatsu N., Hiramoto K., Hirosana T., Hirozana T., Actoh H., Inceani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T., Ratch H., Kawai J., Kojima Y., Kondo S., Konno H., Konda M., Koya S., Katch H., Kawai J., Kojima Y., Kondo S., Konno H., Konda M., Sano H., Nakamura M., Nakamura M., Nakai K., Numazaki R., Ohno M., Obsato N., Obsato N., Osazaki Y., RA Saito R., Saitoh H., Sakai C., Sakai K., Sakaizume N., Sano H., RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M., RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M., RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M., RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y., Submitted (UUL-2011) to the. EMBL/GenBank/DbBJ databases.

C. !- SIMILIARITY: Contains I RING-type zinc finger.

DR HSSP; Q12933; 1CA9.

ROS G0:0004942; Frafezeptor activity; IEA.

GO; G0:0004842; Fraceptor activity; IEA.

GO; G0:0004842; Fraceptor activity; IEA.

GO; G0:0004842; Fraceptor activity; IEA.

BR HGD: MGD: PRO01941; Znf Ting.

InterPro; IPR001941; Znf Ting.

INTERPRO; PR001941; MJTH; I.

R Ffam; PP00197; MJTH; I.

R Ffam; PP00197; MJTH; I.

R Ffam; PP00197; MJTH; I.

R SMART; SM00184; MJTH; I.

R SMART; SM00184; MJTH; I.
SEQUENCE FROM N.A.
STRAINE-2049374; PubMed=1D42159;
Cardinol P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Cardinol P., Shibata Y., Hayatsu N., Hayashizaki Y.;
Konno H., Okazaki Y., Mutamatsu M., Hayashizaki Y.;
Wormalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length CDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=CS7BL/6J; TISSUE=Thymus;

C STRAIN=CS7BL/6J; TISSUE=Thymus;

STRAIN=CS7BL/6J; TISSUE=Thymus;

M EDILINE=20530913; PubMed=11076861;

A MEDILINE=20530913; PubMed=11076861;

A Konno H., Akiyama K., Nagaoka S., Sasaki N., Carninci P., A Konno H., Akiyama K., Kiteunai T., Tashiro H., Itoh M., A Yamamoto R., Matsumoto H., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., A Yoneda Y., Inoue K., Toawa M., Ohara E., Matshiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., A Okazaki Y., Maramatsu M., Inoue Y., Kira A., Hayashizaki Y., "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";
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PROSITE; PS00518; ZF_RING_1; 1.
PROSITE; PS50089; ZF_RING_2; 1.
PROSITE; PS50089; ZF_TRAF; 2.
PROSITE; PS50051; Receptor; Zinc-finger.
SEQUENCE 501 AA; 56026 MW; EB219C117A935FEA CRC64;
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181 KFPMQCKDCGKKKIPREKFLDHSRSCAKSKTACPFSEVGCKVVIDNGKHSDHEQTSVMEH 240
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                                                                                                                                                                                       Gaps
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii, Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Carassius.
NCBI_TaxID=7957;
                                                                                                                                                   Query Match 526; Score 1256; DB 2; Length 526; Best Local Similarity 47.5%; Pred. No. 3.4e-80; Matches 250; Conservative 68; Mismatches 100; Indels 108;
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Wang T., Secombes C.J.;
Submitted (OCT.2000) to the EMBL/GenBank/DDBJ databases.
SIVAILARITY: Contains 1 RING-type zinc finger.
EMBL; AJ297860; CAC82653.1; -..
EMSP; Q12933; 1CZY.
GO; GO:0000151; C:ubiquitin ligase complex; IEA.
GO; GO:0004872; F:receptor activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FLRPNREMNIASGCPLFCPLAKLAGKSSYLRDDTIFIKAIVDLTGL
 SMART; SM00061; MATH; 1.
SMART; SM01084; RING; 1.
PROSITE; PS01089; CYTOCHOME_C; UNKNOWN_1.
PROSITE; PS50144; MATH; 1.
PROSITE; PS50145; ZF_RING_2; 1.
PROSITE; PS50145; ZF_RING_2; 1.
SEQUENCE 526 AA; 59228 WW; DC6D733799E94578 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Tumor necrosis factor receptor associate factor-2.
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                                                      MAAASVTPPGSLELLQPGFSKTLLGTKLEAKYLCSACRNVLRRPFQAQCGHRYCSFCLAS
                                                                                                                                                                                                                                                        --- FQDHVKTCGKCRVPCRFHAIGCLETVEGEKQQEHEVQWL
                      Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
                        79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sou J., Zhang Y., Secombes C.J.;
Submitted (JUN-2003) to the EMEL/GenBank/DDBJ databases.
Submitted (JUN-2003) to the EMEL/GenBank/DDBJ databases.
Submitted (JUN-2003) to the EMEL/GenBank/DDBJ databases.
Structure (Jun-2003) to the EMEL/GenBank/DDBJ databases.
GO; GO:0000151; Configuritin ligase complex; IEA.
GO; GO:0004842; F:ubiquitin ligase activity; IEA.
GO; GO:0008270; F:zeceptor activity; IEA.
GO; GO:0008270; F:zinc ion binding; IEA.
R GO; GO:0016567; P:protein ubiquitination; IEA.
R InterPro; IPR000345; CytC.heme_BS.
InterPro; IPR001841; Znf_ring.
InterPro; IPR001841; Znf_ring.
Pfam: Pp00917; MartH: 1
       Pred. No. 2.2e-126;
; Mismatches 29; Indels
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Tumor necrosis factor receptor associated factor 2.
Name=TRAF2;
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 74.1%; Pred. ww. --
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Pfam; PF00097; zf-C3HC4; 1.
Pfam; PF02176; zf-TRAF; 2.
                      371; Conservative
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Best Local Similarity
Matches 371; Conser
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Klausner R.D., Cellins F.S., Magner L.H., Derge J.G.,
Klausner R.D., Collins F.S., Magner L., Schemmen C.M., Schuler G.D.,
A litechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A litechul S.F., Jordan H., Moore T., Max S.I., Wang J., Hesteh F.,
Diatchenko L., Marushan K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Boneldo M.F., Caraninci P., Frange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abrameon R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Rebey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Rabeeley R.W., Touchman J.W., Green B.D., Dickson M.C.,
Rabeeley R.W., Touchman J.W., Green B.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Jones S.J., Marra M.A.,
Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W., Richardson P.;
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Xlein S., Straubberg R.;
Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.

REST (MATCHARITY: Contains 1 RING-type zinc finger.
RICEPTO; IPR002083; MATH.
RICEPTO; IPR001841; Znf_Ting.
RICEPTO; IPR001841; Znf_TRAF.
REST (MACHARIA) (MATH) 1.
REST (MACHARIA) (MACHARI
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MEDLINE=22341132; PubMed=12454917; Medline=22341132; PubMed=12454917;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 52.0%; Score 1149.5; DB 2; Length 501; Local Similarity 47.6%; Pred. No. 1e-72; es 226; Conservative 60; Mismatches 84; Indels 105;
GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
GO; GO:0008270; F:zinc ion binding; IEA.
GO; GO:0008567; P:protein ubiquitination; IEA.
InterPro; IPRO0803; MATH.
InterPro; IPRO0804; Traf like.
InterPro; IPRO0804; Traf like.
InterPro; IPRO08023; Znf Traf like.
InterPro; IPRO0129; Znf Traf like.
INTER PRO0175; Znf Like.
INTER PRO0175; Znf Traf like.
INTER PRO0175; Znf Like.
INTER PRO0175; Znf Like.
INTER PRO0175; Znf Like.
INTER PRO0175; Znf Like.
                 F:ubiquitin-protein ligase activity; IEA.
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                                                                                                                                LSSGPONCAACVHEGIYEEGISILESSSAFPDNAARREVESLPAVCPSDGCTWKGTLKEY
                                                                                           7 AAVSVSPQGSLDLNQPGFKKEILGTKLEVKYLCSDCKNLIRRPLQAQCGHRYCSHCFSKI
                                                                 2 AAASVTPPGSLELLQPGFSKTLLGTKLEAKYLCSACRNVLRRPFQAQCGHRYCSFCLASI
                                105;
   DB 2; Length 461;
51.2%; Score 1131.5; DB 2; Length 49.1%; Pred. No. 1.7e-71; ive 56; Mismatches 70; Indels
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             Best Local Similarity 49.1
Matches 223; Conservative
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Xenopus laevis (African clawed frog). Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae;

SEQUENCE FROM N.A. TISSUE=Oocytes; MEDLINE=22388257; PubMed=12477932;

Xenopodinae; Xenopus.
NCBI_TaxID=8355;

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Created)
Last sequence update)
Last annotation update)

05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, MGC83471 protein.

PRELIMINARY;

-ELLQRCESL 196

AAH70713

RESULT 11 AAH70713

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127 EVGHEGKCQFMLVPCPVCKALIRAIDRDLHNERECPERKLNCRYCKLSVYFPDIKVHDEI 186
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                                                                                                                                                                                                                             187 CPKFPWTCEGCGRKKIPREKFQDHIKGCGRCKVPCRYAAVGCAEMVENDKCLEHENKFLA 246
                                                                                                                                                                                                                                                                                                                       247 EHLAKVWDYIQRDIKEQKDLLLRVGSLSVQGSSTPGHNALPVPPNDSTKVKEILQKLDTL 306
                                                                                                                                                                                                                                                                                                                                                            EKKTATFENIVCVLNREVERVAMTAEACSRQHRLDQDKIEALSSKVQQLERSIGLKDLAM 256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 AAVSVSPQGSLDLNQPGFKKEILGTKLEVKYLCSDCKNLLRRPLQAQCGHRYCSHCFSKI 66
                                             LSSGPQNCAACVHEGIYEEGISILESSSAPPDNAARREVESLPAVCPSDGCTWKGTLKEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marundina K., Farmer A.A., Rubin G.M., Hong L., Diatchenko L., Marundina K., Farmer A.A., Rubin G.M., Hong L., Brapteton M., Scares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRAI_HUMAN STANDARD; PRT; 416 AA.
Q13077; QBNF13;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2004 (Rel. 44, Last annotation update)
TNF receptor associated factor 1 (Epstein-Barr virus-induced protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mosialos G., Birkenbach M., Yalamanchili R., VanArsdale T., Ware C.,
Kieff B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The Epstein-Barr virus transforming protein LMP1 engages signaling proteins for the tumor necrosis factor receptor family."; Cell 80:389-399(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606,
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TISSUE=Spleen;
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AAH70713;
AAH70713;
AAH70713;
AAH70713;
AAH70713;
AAY-2004 (TEBMBLrel. 27, Last sequence update)
AAY-2004 (TEBMBLrel. 27, Last sequence update)
AAY-2004 (TEBMBLrel. 27, Last annotation update)
Hypothetical protein.
AFOODUS laevis (African clawed frog).
AEODUS laevis (African Clawed frog).
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
AEODOGInae; Xenopus; Xenopus.
ANCBI_TAXID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 51.2%; Score 1131.5; DB 2; Length 461; Best Local Similarity 49.1%; Pred. No. 1.7e-71; Matches 223; Conservative 56; Mismatches 70; Indels 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Klein S., Strausberg R.;
Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC070713; AAH70713.1; -.
Hypothetical protein:
SEQUENCE 461 AA; 51826 MW; 9981DC4C003C321D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    roc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                         LNGDGTGRGTHLSLFFVVMKGPNDALLRWPFNQK 350
                                                                                                                                                              461 AA.
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MEDLINE=22341132; PubMed=12454917;
MEDLINE=22341132; PubMed=12454917;
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MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dev. Dyn. 225:384-391(2002).
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                                                                                                                                                                                                                                                                                 PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Klein S.L.,
Richardson
                                                                                                                                       317
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Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Mazny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
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the CD30 cytoplasmic domain in association with tumor necrosis factor
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Goeddel D.V.;
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Pullen S.S., Miller H.G., Everdeen D.S., Dang T.T., Crute J.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=21519158; PubMed=11607847; DOI=10.1038/sj/onc/1204788;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INTERACTION WITH INFRSF8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INTERACTION WITH TANK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cell 78:681-692(1994)
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MEDLINE=21264720; PubMed=11035039; DOI=10.1074/jbc.M008356200;
MEDLINE=21264720; PubMed=11035039; DOI=10.1074/jbc.M008356200;
MEDLINE=21264720; PubMed=11035039; DOI=10.1074/jbc.M008356200;
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transpale, JNK, and cell death pathways and binds to ectodysplasin A.";
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M. M. Mandara mod kinases. Mediates activation of NF-kappa-B and JNK and is involved in apoptosis. The TRAFI/TRAFZ complex recruits the apoptosic suppressors BIRC2 and BIRC3 to TNFRSPIB/TNFR2.
M. SUBUNT: Homotrimer (Probable). Heteromer with TRAFZ and associates with TNFRSFIB/TNFR2 through TRAFZ. Associates with
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Hatzoglu A., Roussel J., Bourgeade M.-F., Rogier E., Madry C.,
Inoue J.-I., Dovergne O., Tspis A.; Rogier E., Madry C.,
Trone J.-I., Dovergne O., Tspis A.; Rogier E., Madry C.,
Trone J.-I., Roussel J., Rogie B.,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INTERACTION WITH INFRSF19L.

MEDILINE=12131541; PubMed=11313261;

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MEDIATE=99156876; PubMed=10037686;
MEDIATE=99156876; PubMed=10037686;
Kwon B., Yu K.-Y., Ni J., Yu G.-L., Jang I.-K., Kim Y.-J., Xing L.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  "CD28-independent, TRAF2-dependent costimulation of resting T cells 4-1BB ligand.";
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MEDLINE=20370246; PubMed=10809768;
MEDLINE=20370246; PubMed=10809768;
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factors and activate nuclear factor kappaB.";
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MEDILINE=98270944, PubMed=6607925,
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Goldstein M.D., Bangia N., DeBenedette M.A., Mak T.W., Choi Y.,
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Wong B.R., Josien R., Lee S.Y., Vologodskaia M., Steinman R.M.,
Choi Y.;
INTERACTIONS WITH TWFRSF4 AND TWFRSF9.
MEDLINE=98078711; PubMed=9418902;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INTERACTION WITH TNFRSF11A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Watts T.H.;
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82 ------AEAGIGCPFAGVGCSFKGSPQSVQEHEVTSQTSHLNLLL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        170 SSVLEAKPLLGDQSHAGSELLQR------ 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GFMKQWKARLGCGLESGPMALEONLSDLQLQAAVEVAGDLEVDCYRAPCSESQEELALQH 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    247 RSIGLKDLAMADLEQKVLEMEASTYDGVFIWKISDFARKLQEAVAGRIPAIFSPAFYTSR 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301 YGYKLCLKLYLNGDGTGKRTHLSLFIVIMRGEYDALLPWPFRNKVTFMLLDQNNREHAID 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YGYKMCLRIYLNGDGTGRGTHLSLFFVVMKGPNDALLRWPFNQKVTLMLLDQNNREHVID 366
                                                                                                                                                                                                                                                                                                                                                                                                                     81
                                                                                                                                                                                                                                                                                                                                                                              55 SFCLASILSSGPON-----CAACVHEGIYEEGISILESSSAFPDNAARREVESLPAVCPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     195 -----SLEKKTATFENIVCVLNREVERVAMTAEACSRQHRLDQDKIEALSSKVQQLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           110 DGCTWKGTLKEYEFQDHVKTCGKCRVPCRFHAIGCLETVBGEKQQEHEVQWLREHLAMLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRA3 MOUSE STANDARD; PRT; 567 AA.

060803; 062380;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
1TNF receptor associated factor 3 (CD40 receptor associated factor 1)
(CRAF1) (TRAFAMN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEGUENCE FROM N.A., AND INTERACTION WITH TNPRSFS.
MEDLINE=95184010; PubMed=7533327;
Cleary A.M., Ye Z., Hong D.I., Lederman S., Baltimore D.;
"Involvement of CRAR!, a relative of TRAF, in CD40 signaling.";
Science 267:1494-1498(1995).
TNFRSF1, TNFRSF5/CD40, TNFRSF8/CD30, TNFRSF9/CD137, TNFRSF11A/RANK, TNFRSF19/BCMA, TNFRSF19/TROY, TNFRSF19L/RELT, XEDAR, EDAR, EDStein-Barr virus BNFL1/LMP-1, TANK/ITRAF, TRAIP and RIPK2. Interacts with BIRC2 and BIRC3 N-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        367 APRPDVTSSSFORPVNDMNIASGCPLFCPVSKMEA-KNSYVRDDAIFIKAIVD 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Musimae, Mus
                                                                                                                                                                                                                                                                                                                                           83;
                                                                                                                      oligomerization.
DOMAIN: The MATH/TRAF domain binds to receptor cytoplasmic
                                                                                                   DOMAIN: The coiled coil domain mediates homo- and hetero-
                                                                                                                                                                            -!- SIMILARITY: Contains 1 MATH domain.
-!- CAUTION: Ref.2 sequence differs from that shown due to a frameshift in position 111.
                                                                                                                                                                                                                                                                                                     DB 1; Length 416;
                                                                                                                                                                                                                                                                                                   33.2%; Score 733.5; DB 1; Length 4 llarity 37.8%; Pred. No. 1.8e-43; Conservative 65; Mismatches 109; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
STRAIN=C57BL/6J; TISSUE=Brain;
MEDLINE=96299439; PubMed=8660894;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=Traf3; Synonyms=CRAF1, Trafamn;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                 terminus.
                                                                                                                                                                domains.
                                                                                                                                                                                                                                                                                                                                      156;
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Dimulos M.B., Disteche C.M., Copeland N.G., Gilbert D.J.,

A Jenkins N.A., Lacy E.;

"A candidate gene for the amnionless gastrulation stage mouse mutation

"A candidate gene for the amnionless gastrulation stage mouse mutation

"A candidate gene for the amnionless gastrulation stage mouse mutation

"E candidate gene for the amnionless gastrulation stage mouse mutation

"E code a TRAF-related protein and signal transducer that links members

"C of the tumor necrosis factor receptor family to different

signaling pathways by association with the receptor cytoplasmic

domain and kinases. Seems to be involved in activation of NF-

kappa-a and JNK and in apoptosis. Is regulated by TANK/ITRAF which

competes with TNRRSFS/CD40 for binding. Seems to play a role T-

cell dependent immune responses (By similarity).

"Similarity). Binds to TNRRSFS/CD40. Associates with LTBR/NTRRSF3,

TNFRSF4, TNRRSF8/CD30, TNFRSF17/BCMA and EDAR, MAP3K5, MAP3K14,

and TRAF-interacting protein TRIP and TRAF and TNF receptor

associated protein TTRAP. Binds to TANK/ITRAF (By similarity).

"ITSSUE SPECIFICITY: In adult, highest in brain. Also found in

kidney, heart, thymus, spleen, lung, muscle, testis and ovary. Not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 MDAAGTLQPNPPLKLQPDRGAGSVLVPEQGGYKEKFVKT-VEDKYKCEKCRLVLCNPKQT 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MAAASVTPPGSLELLQP-----GFSKTLLGTKLEAKYLCSACRNVLRRPFQA 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEVELOPMENTAL STAGE: In the embryo, expressed from E6.5 with highest levels found between E11.5 and E13.5. At late stages of gestation, from E14.5, only low levels are detected. DOWAIN: The MATH/TRAF domain binds to receptor cytoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32.1%; Pred. No. 4.7e-43; ive 80; Mismatches 131; Indels 184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33.0%; Score 730; DB 1; Length 567; 32.1%; Pred. No. 4.7e-43;
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2522B343B41192DC CRC64;
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TRAF-type 1.
TRAF-type 2.
Coiled coil (Potential).
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-1- SIMILARITY: Contains 1 RING-type zinc finger.
-1- SIMILARITY: Contains 2 TRAF-type zinc fingers.
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PROSITE; PS00518; ZF RING 1; 1.
PROSITE; PS50089; ZF RING 2; 1.
PROSITE; PS50145; ZF TRAF; 2.
Apoptosis; Colled coll; Repeat; Zinc-finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MSD: 033940; MAC221011; ...
HSSP; Q13114; 1FLK.
MGD; MG1:108041; Traf3.
InterPro; 1PR002083; MATH.
InterPro; 1PR008974; Traf like.
InterPro; 1PR001841; Znf ring.
InterPro; 1PR001841; Znf ring.
Fam; PF00317; MATH; 1.
Pfam; PF00317; MATH; 1.
Pfam; PF00317; Zf-C3HC4; 1.
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SMART; SM00184; RING; 1
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390
367 AA;
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Matches 187; Conserv
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130
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                                                                                                                                                                                                                                               ----CRFHAI 142
                                                                                                                                                                                                                                                                                                      SHCKSQVPMIKLQKHEDTDCPCVVVSCPHKCSVQTLLRSELSAHLSECVNAPSTCSFKRY 236
                                                                                                                                                                                                                                                                                                                                                                 GCLETVEGEKQQ--EHEVQWLREHLAML--LSSVLEAKPLLGDQSHAGSELLQRCESLEK 198
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QCGHRYCSFCLASILSSGPQNCAACVHEGIYEEGISILESSSAFPDNAARREVESLPAVC 107
                                                             ----FKDNCCKREILALQVYC 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KVLEMEASTYDGVFIWKISDFARKLQEAVAGRIPAIFSPAFYTSRYGYKMCLRIYLNGDG 321
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STRANN=C5PBL/6J; TISSUE=Skin;
The FANTOM CORSORTIUM,
The RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation 60,770 full-length cDNAs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Mus musculus 10 days neonate skin cDNA, RIKEN full-length enriched
library, clone:4732496E14 product:Thf receptor-associated factor 1,
full insert sequence.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     381 VNDMNIASGCPLFCPVSKMEAKNSYVRDDAIFIKAIVDLTGL
                                      ECGHRECESCMAALLSSSSPKCTAC-QESIIKDKV---
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MEDLINE=9279223; PubbMed=10349636;
Carninci P., Hayshizaki Y.;
"High-efficiency full-length cDNA cloning.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           409 AA,
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                                                                                                                       PSD--GCTWKGTL------KEYEFQ---
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STRAIN=CSPIL/60; TISSUE=Skin;
MEDLINE=21085660; Pubmed=11217851;
RIKEN FANTOM CONSORTHUM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Meth. Enzymol. 303:19-44(1999).
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Adachi J., Alzawa K., Akimura T., Arakawa T., Bono H., Carninci P.,

Adachi J., Alzawa K., Akimura T., Arakawa T., Bono H., Carninci P.,

Brukuda S., Furuno M., Harancto K., Hiracka T., Hirozane T.,

Hayashida K., Hayatsu N., Hiracha T., Kasukawa T.,

Attoh H., Kawai J., Kojima Y., Kondo S., Konno H., Konda M., Koya S.,

Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Nasawa T.,

Katoh H., Kawai T., Kojima Y., Kondo S., Konno H., Nakamura M.,

Nishi K., Nomura K., Numazaki A., Murata M., Nakamura M.,

Nishi K., Nomura K., Numazaki C., Sakai K., Sakazume N., Sano H.,

Sasaki D., Shibata K., Shinaqawa A., Shiraki T., Soqabe Y., Taqami M.,

Taqawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,

Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;

Submitted (Jul-2001) to the EMBL/GenBank/DDBJ databases.
                                                         STRAIN=CS7BL/6J; TISSUE=Skin;

MEDILINE=2049374; PLMSG=11042159;

MEDILINE=2049374; PLMSG=11042159;

Carminci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itch M.,

Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;

"Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new genes.";

Genome Res. 10:1617-1630(2000).
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                                                                                                                                                                                                                                       STRAIN=C57BL/64); TISSUB=Skin,
MEDLINE=20530913; PubMed=11076861;
Shibata K, Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P.,
Shibata K, Itoh M., Alzawa K., Kitsumai T., Tashiro H., Itoh M.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watshiki M.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
Rikis integrated sequence analysis (RISA) system-384-format
Genome Res. 10:1757-1771(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       409 AA; 45464 MW; ADD7F997169D9AAD CRC64;
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GO; GO:0004872; F:receptor activity; IEA.
InterPro; IPR0022083; MATH.
Pfam; PP00917; MATH; I.
SMART; SM00061; MATH; I.
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Nature 420:563-573(2002).
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SEQUENCE
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MEDLINE=97258620; PubMed=9104814;
Lee S.Y., Lee S.Y., Choi Y.;
Lee S.Y., Lee S.Y., Choi Y.;
The lee S.Y., Lee S.Y., Choi Y.;
The lee S.Y., Lee S.Y., Choi Y.;
Lee S.Y., Lee S.Y., Choi Y.;
The lee S.Y., Lee S.Y., Choi Y.;
The lee S.Y., Lee S.Y., Choi Y.;
The lee S.Y., Lee S.Y., Choi Y.;
The lee S.Y., Lee S.Y., Choi Y.;
The lee S.Y., Lee S.Y., Choi Y.;
The lee S.Y., Lee S.Y., Choi Y.;
The lee S.Y., Lee S.Y., Choi Y.;
The lee S.Y., Lee S.Y., Choi Y.;
The lee S.Y., Lee S.Y., Choi Y.;
The lee S.Y., Lee S.Y., Choi Y.;
The lee S.Y., Lee S.Y., Choi Y.;
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The lee S.Y., Lee S.Y., Choi Y.;
The lee S.Y., Lee S.Y., Choi Y.;
The S.Y., Choi Y.;
The S.Y., Lee S.Y., Choi Y.;
The S.Y., Ch
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                                                 371
                                                                                299 CLRLYLNGDGSGKKTHLSLFIVIMRGEYDALLPWPFRNKVTFWLLDQNNREHAIDAFRPD 358
298
239 KDQVLGKLEHSLRLMEEASFDGTFLWKITNVTKRCHESVCGRTVSLFSPAFYTAKYGYKL
                                                    312 CLRIYLNGDGTGRGTHLSLFFVVMKGPNDALLRWPFNQKVTLMLLDQNNREHVIDAFRPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., SEQUENCE OF 123-135 AND 390-402, AND INTERACTIONS WITH TRAFZ AND THREACESTB.
MEDLINE-94349371; Pubmed=86069916;
Rothe M., Wong S.C., Henzel W.J., Goeddel D.V.;
"A novel family of putative signal transducers associated with the cytoplasmic domain of the 75 kDa tumor necrosis factor receptor.";
cell 78:681-692(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eucheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBL_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  oligomerization.
DOMAIN: The MATH/TRAF domain binds to receptor cytoplasmic
                                                                                                                                                                                    359 LSSASFQRPQSETNVASGCPLFFPLSKLQSPKHAYVKDDTMFLKCIVD 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: Cytoplasmic.
DOMAIN: The coiled coil domain mediates homo- and hetero-
                                                                                                                                                     372 VISSSFQRPVNDMNIASGCPLFCPVSKMEA-KNSYVRDDAIFIKAIVD
                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
02-UL-2004 (Rel. 44, Last annotation update)
TNF receptor associated factor 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: Contains 1 MATH domain.
                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INTERACTION WITH TRAIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                              TRA1 MOUSE
P39428;
                                                                                                                                                                                                                                                                                     RESULT 15
TRA1 MOUSE
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EMBL; L35302; AAC37663.1; PIR; A54750; A54750. HSSP; Q12933; 1CZY. MGD; MGI:101836; Traf1. InterPro; IPR002083; MATH

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9
                                                                                                                                                                                                                                                                                                                            85 LESSSAFPDNAARREVESLPAVCPSDG----CTWKGTLKEYEFQDHVKTCGKCR----- 134
                                                                                                                                                                                                                                                                                                                                                                                                                           -----VPCRFHAIGCLETVEGEKQQEHEVQWLREHLAMLLSSVLE 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59 VSPGSPLTQEKVHSDVAEAEIMCPFAGVGCSFKGSPQSMQEHEATSQSSHLYLLLAVLKE 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            119 WKSSPGSNLGSAPMALERNLSELQLQAAVEATGDLEVDCYRAPCCESQEELALQHLVKEK 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KOLAMADLEQKVLEMEASTYDGVFIWKISDFARKLOEAVAGRIPAIFSPAFYTSRYGYKM 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLRIYLNGDGTGRGTHLSLFFVVMKGPNDALLRWPFNQKVTLMLLDQNNREHVIDAFRPD 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            299 CLRLYLNGDGSGKKTHLSLFIVIMRGEYDALLPWPFRNKVTFMLLDQNNREHAIDAFRPD 358
                                                                                                                                                                                                                                                                                                                                                    196 ----LEKKTATFENIVCVLNREVERVAMTAEACSROHRLDODKIEALSSKVOOLERSIGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                             16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 418
                                                                                                                                                                                                                        Length 409;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        359 LSSASFQRPQSETNVASGCPLFFPLSKLQSPRHAYVKDDTMFLKCIVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              372 VTSSSFORPVNDMNIASGCPLFCPVSKMEA-KNSYVRDDAIFIKAIVD
                                                                                                                                                                                                                        32.9%; Score 727; DB 1; Length 40: 38.5%; Pred. No. 5.1e-43; ive 63; Mismatches 112; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             175 AKPLIGDQSHAGSELLQR----CES
                                                                                                                                                                        EBA7FEES639FEDDF CRC64;
InterPro; IPR008974; Traf_like.
Pfam, PR00917, MATH; 1.
PROSITE; PS50144; MATH; 1.
Apoptosis; Coiled coll; Direct protein sequencing.
DOMAIN 167 256 Coiled coll (Potential).
DOMAIN 259 405 MATH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search completed: November 10, 2004, 16:28:16
                                                                                                                                                                           409 AA; 45464 MW;
                                                                                                                                                                                                                     Query Match
Best Local Similarity 38.5%
Matches 157, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                              135 -----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Job time : 200 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  312
                                                                                                                                                                           SEQUENCE
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